

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: October 22, 2002, 14:18:02 ; Search time 1789 Seconds  
(without alignments)  
12703.308 Million cell updates/sec

Title: US-09-374-967-1  
Perfect score: 1086  
Sequence: 1 atgaagggccctatcttctgt.....agcctgagatcgtcatgtga 1086

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Optimal number of hits satisfying chosen parameters: 517008

Minimum DB seq length: 20  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 1000 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vi:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
73	17.4				
72	17.4				
71	17.4				
70	17.4				
69	17.4				
68	17.6				
67	17.6				
66	17.6				
65	17.6				
64	17.6				
63	17.6				
62	17.6				
61	17.6				
60	17.6				
59	17.6				
58	17.6				
57	17.6				
56	17.6				
55	17.6				
54	17.6				
53	17.6				
52	17.6				
51	17.6				
50	17.6				
49	17.8				
48	17.8				
47	17.8				
46	17.8				
45	17.8				
44	17.8				
43	17.8				
42	18				
41	18				
40	18				
39	18				
38	18				
37	18				
36	18				
35	18.2				
34	18.2				
33	18.2				
32	18.2				
31	18.2				
30	18.4				
29	18.4				
28	18.4				
27	18.6				
26	18.6				
25	18.6				
24	18.6				
23	18.6				
22	18.6				
21	18.6				
20	18.6				
19	18.6				
18	18.6				
17	18.8				
16	18.8				
15	18.8				
14	19				
13	19.2				
12	19.4				
11	19.4				
10	19.4				
9	19.4				
8	19.4				
7	19.4				
6	19.6				
5	20.2				
4	20.2				
3	20.2				
2	20.6				
1	21.2				

42	6	AR021485	AR021485 Sequence
45	6	AR085813	AR085813 Sequence
45	6	A05545	A05545 Oligonucleo
45	6	AR001638	AR001638 Sequence
45	6	109095	109095 Sequence
27	6	AX116244	AX116244 Sequence
37	6	HSU26584	HSU26584 Sequence
47	6	155815	155815 Sequence
47	6	A23295	A23295 Sequence
49	6	103151	103151 Sequence
48	6	125130	125130 Sequence
35	6	AX155571	AX155571 Sequence
10	6	AF071633	AF071633 Mus muscu
29	6	A08855	A08855 Sequence
34	6	AX202646	AX202646 Sequence
45	9	S77758	S77758 Homo sapien
28	6	AR145872	AR145872 Sequence
34	6	AR142300	AR142300 Sequence
34	6	127173	127173 Sequence
34	6	132754	132754 Sequence
38	6	AX273757	AX273757 Sequence
45	6	AR030770	AR030770 Sequence
45	6	AR101774	AR101774 Sequence
50	6	AR027899	AR027899 Sequence
50	6	AX207611	AX207611 Sequence
40	6	A05823	A05823 Oligonucleo
12	6	SYNHYGROAI	SYNHYGROAI
40	6	A05822	A05822 Oligonucleo
42	6	AR069155	AR069155 Sequence
42	6	149576	149576 Sequence
47	6	BD006283	BD006283 Artificial
50	6	AX164918	AX164918 Sequence
50	6	AX199520	AX199520 Sequence
45	6	AR032422	AR032422 Sequence
45	6	129162	129162 Sequence
45	6	190836	190836 Sequence
45	6	HSAR24254	HSAR24254 Homo sapi
50	6	AR032803	AR032803 Sequence
50	6	129543	129543 Sequence
50	6	191217	191217 Sequence
30	6	A39884	A39884 Sequence
30	6	AR021165	AR021165 Sequence
36	6	189304	189304 Sequence
39	6	E17102	E17102 Primer. 7/1
44	6	A65462	A65462 Sequence
48	6	183399	183399 Sequence
45	6	AX222136	AX222136 Sequence
38	6	AR066502	AR066502 Sequence
38	6	160026	160026 Sequence
40	6	AR07089	AR07089 Sequence
40	6	AR07159	AR07159 Sequence
41	6	AR07075	AR07075 Sequence
41	6	AR07097	AR07097 Sequence
41	6	AR07119	AR07119 Sequence
43	6	AR07143	AR07143 Sequence
43	6	AX297557	AX297557 Sequence
44	6	AR116487	AR116487 Sequence
44	6	AR116489	AR116489 Sequence
45	6	AR096677	AR096677 Sequence
45	6	HSAR293224	HSAR293224 Homo sapi
45	10	MMTCRAIK	MMTCRAIK
45	6	AX32643	AX32643 Sequence
46	6	129383	129383 Sequence
46	6	191057	191057 Sequence
46	6	AR148158	AR148158 Sequence
33	6	E11460	E11460 Sequence
36	6	E02236	E02236 Synthetic D
38	6	AX228424	AX228424 Sequence
41	6	AR109116	AR109116 Sequence
42	9	HSU30436	HSU30436 Human isola

74	17.4	1.6	43	6	AR061653	AR061653 Sequence	C 147	16.8	1.5	46	6	AR096675	AR096675 Sequence
75	17.4	1.6	43	6	AR108552	AR108552 Sequence	C 148	16.8	1.5	47	6	AX114337	AX114337 Sequence
76	17.4	1.6	43	6	I16509	Sequence 33	C 149	16.8	1.5	47	6	I08398	I08398 Sequence 20
77	17.4	1.6	43	6	I66995	Sequence 33	C 150	16.8	1.5	48	6	AR028619	AR028619 Sequence
78	17.4	1.6	43	6	I85089	Sequence 33	C 151	16.8	1.5	48	6	AX018731	AX018731 Sequence
79	17.4	1.6	45	3	PAPPHOSC	AX167446 Sequence	C 152	16.8	1.5	50	1	MLSPCPI	X16529 Micrococcus
80	17.4	1.6	45	3	AX159876	Sequence	C 153	16.8	1.5	50	6	E59808	E59808 Method for
81	17.4	1.6	29	6	E08133	AX159876 Sequence	C 154	16.8	1.5	50	10	MMU41922	U41922 Mus musculus
82	17.2	1.6	29	6	AR021053	E08133 DNA encodin	C 155	16.6	1.5	23	6	AR095445	AR095445 Sequence
83	17.2	1.6	34	6	AR021056	AR021053 Sequence	C 156	16.6	1.5	23	6	E16761	E16761 Primer. 7/1
84	17.2	1.6	34	6	AR043468	AR043468 Sequence	C 157	16.6	1.5	24	6	AX290635	AX290635 Sequence
85	17.2	1.6	34	6	AR043471	Sequence	C 158	16.6	1.5	31	6	AR048517	AR048517 Sequence
86	17.2	1.6	34	6	AR063383	Sequence	C 159	16.6	1.5	31	6	AX203807	AX203807 Sequence
87	17.2	1.6	34	6	AR062386	Sequence	C 160	16.6	1.5	33	6	AR129902	AR129902 Sequence
88	17.2	1.6	37	6	AR016399	Sequence	C 161	16.6	1.5	33	6	AR148203	AR148203 Sequence
89	17.2	1.6	37	6	AR019257	Sequence	C 162	16.6	1.5	33	6	BD000739	BD000739 Method fo
90	17.2	1.6	37	6	AX223039	Sequence	C 163	16.6	1.5	33	6	E53378	E53378 Thermoslabl
91	17.2	1.6	37	6	AR009896	AX223039 Sequence	C 164	16.6	1.5	33	23	E10233	E10233 Synthetic O
92	17.2	1.6	40	6	AR109102	Sequence	C 165	16.6	1.5	33	23	E10927	E10927 Primer. 9/2
93	17.2	1.6	41	6	AX022217	Sequence	C 166	16.6	1.5	33	23	E10942	E10942 Synthetic O
94	17.2	1.6	41	6	AX030743	Sequence	C 167	16.6	1.5	36	6	AR060414	AR060414 Sequence
95	17.2	1.6	41	6	AX214512	Sequence	C 168	16.6	1.5	36	6	AR120420	AR120420 Sequence
96	17.2	1.6	41	6	BD008658	BD008658 Strable ex	C 169	16.6	1.5	36	6	AR128972	AR128972 Sequence
97	17.2	1.6	41	6	E07492	Sequence	C 170	16.6	1.5	36	6	I03346	I03346 Sequence 4
98	17.2	1.6	42	6	AR035926	Sequence	C 171	16.6	1.5	36	6	I06587	I06587 Sequence 13
99	17.2	1.6	45	6	I20162	Sequence	C 172	16.6	1.5	36	6	I06588	I06588 Sequence 14
100	17.2	1.6	45	6	AR038995	Sequence	C 173	16.6	1.5	36	6	I61943	I61943 Sequence 49
101	17.2	1.6	48	6	AR107387	Sequence	C 174	16.6	1.5	37	6	AX220122	AX220122 Sequence
102	17.2	1.6	48	6	S81647	TCR beta V8	C 175	16.6	1.5	38	6	AX222689	AX222689 Sequence
103	17.2	1.6	48	10	ECOINSX	AX107387 Sequence	C 176	16.6	1.5	38	6	A63066	A63066 Sequence 10
104	17.2	1.6	49	1	AX103394	Sequence	C 177	16.6	1.5	40	6	I18925	I18925 Sequence 11
105	17.2	1.6	49	6	AX166826	Sequence	C 178	16.6	1.5	40	9	HS274595	Z74595 H.sapiens 5
106	17.2	1.6	49	6	AX156795	Sequence	C 179	16.6	1.5	40	12	SYN5V4FLN2	K02762 SYA40 Late r
107	17.2	1.6	50	6	AX190220	Sequence	C 180	16.6	1.5	40	9	E06337	E06337 Primer. 9/1
108	17.2	1.6	50	6	E25625	AX156795 Sequence	C 181	16.6	1.5	41	6	E06533	E06533 Primer. 9/1
109	17.2	1.6	50	6	E27175	RNA-DNA chl	C 182	16.6	1.5	41	6	I06319	I06319 Sequence 4
110	17.2	1.6	28	6	E04870	Synthetic D	C 183	16.6	1.5	42	6	HSC085712	HSC085712 Sequence
111	17.2	1.6	33	6	E04870	Protein hav	C 184	16.6	1.5	44	6	AX136036	AX136036 Sequence
112	17.2	1.6	33	6	E63914	Sequence	C 185	16.6	1.5	44	6	BD006871	BD006871 OligonucL
113	17.2	1.6	35	11	C75689	Sequence	C 186	16.6	1.5	44	6	AX180733	AX180733 Sequence
114	17.2	1.6	35	11	HPBREC8B	Sequence	C 187	16.6	1.5	45	6	AX180855	AX180855 Sequence
115	17.2	1.6	41	6	AR4797	Sequence 2	C 188	16.6	1.5	45	6	AR019541	AR019541 Sequence
116	17.2	1.6	41	6	I04548	Sequence 10	C 189	16.6	1.5	45	6	AR019541	AR019541 Sequence
117	17.2	1.6	44	5	GGU62254	U62254 Gallus gall	C 190	16.6	1.5	45	6	HSTRK1	HSTRK1 Sequence
118	17.2	1.6	44	6	AX199548	Sequence	C 191	16.6	1.5	46	6	AR032556	AR032556 Sequence
119	17.2	1.6	45	6	AR011231	Sequence	C 192	16.6	1.5	46	6	I29296	I29296 Sequence 16
120	17.2	1.6	45	6	AR125138	Sequence	C 193	16.6	1.5	46	6	I47747	I47747 Sequence 19
121	17.2	1.6	45	6	I17869	Sequence 99	C 194	16.6	1.5	47	6	I49026	I49026 Sequence 35
122	17.2	1.6	48	6	I20582	Sequence 17	C 195	16.6	1.5	47	6	A39830	A39830 Sequence 3
123	17.2	1.6	48	6	I24206	Sequence 28	C 196	16.6	1.5	47	6	A62658	A62658 Sequence 22
124	17.2	1.6	50	3	G1AC264	I49334 SRS of NotI	C 197	16.6	1.5	49	6	AR044011	AR044011 Sequence
125	17.2	1.6	50	3	I42290	Sequence 10	C 198	16.6	1.5	49	6	AR038187	AR038187 Sequence
126	17.2	1.6	50	6	HPBHDWIN2	K01660 Hepatitis B	C 199	16.6	1.5	49	6	AR044011	AR044011 Sequence
127	17.2	1.6	50	6	AR070760	Sequence	C 200	16.6	1.5	50	6	AR044011	AR044011 Sequence
128	16.8	1.5	24	6	AR122966	Sequence	C 201	16.6	1.5	50	6	AR044011	AR044011 Sequence
129	16.8	1.5	24	6	BD005402	Protein 1	C 202	16.6	1.5	50	6	AR044011	AR044011 Sequence
130	16.8	1.5	26	6	AR043520	Sequence	C 203	16.6	1.5	50	6	AR044011	AR044011 Sequence
131	16.8	1.5	26	6	I59662	Sequence 6	C 204	16.6	1.5	50	6	AR044011	AR044011 Sequence
132	16.8	1.5	26	6	AR172434	Sequence	C 205	16.6	1.5	50	6	AR044011	AR044011 Sequence
133	16.8	1.5	29	6	AR172434	Sequence	C 206	16.6	1.5	50	6	AR044011	AR044011 Sequence
134	16.8	1.5	33	6	E16104	PCR Primer	C 207	16.6	1.5	50	6	AR044011	AR044011 Sequence
135	16.8	1.5	36	6	AX218854	Sequence	C 208	16.6	1.5	50	6	AR044011	AR044011 Sequence
136	16.8	1.5	39	6	E40309	Novel prote	C 209	16.6	1.5	50	6	AR044011	AR044011 Sequence
137	16.8	1.5	40	6	A35758	Synthetic o	C 210	16.6	1.5	50	6	AR044011	AR044011 Sequence
138	16.8	1.5	40	6	AR169006	Sequence	C 211	16.6	1.5	50	6	AR044011	AR044011 Sequence
139	16.8	1.5	42	6	A09950	Sequence	C 212	16.6	1.5	50	6	AR044011	AR044011 Sequence
140	16.8	1.5	42	6	E39990	Antibody fo	C 213	16.6	1.5	50	6	AR044011	AR044011 Sequence
141	16.8	1.5	43	6	AR104022	Sequence	C 214	16.6	1.5	50	6	AR044011	AR044011 Sequence
142	16.8	1.5	43	6	AR104055	Sequence	C 215	16.6	1.5	50	6	AR044011	AR044011 Sequence
143	16.8	1.5	43	6	AR104056	Sequence	C 216	16.6	1.5	50	6	AR044011	AR044011 Sequence
144	16.8	1.5	43	6	AR104057	Sequence	C 217	16.6	1.5	50	6	AR044011	AR044011 Sequence
145	16.8	1.5	43	6	I27076	Sequence 18	C 218	16.6	1.5	50	6	AR044011	AR044011 Sequence
146	16.8	1.5	44	10	MMTCRAEPI	X70724 M.musculus	C 219	16.6	1.5	50	6	AR044011	AR044011 Sequence

C 220	16.4	1.5	36	6	AR031346	AR031346 Sequence	C 293	16.2	1.5	39	6	AX232229	AX232229 Sequence
C 221	16.4	1.5	36	6	AR062478	AR062478 Sequence	C 294	16.2	1.5	40	6	AR035910	AR035910 Sequence
C 222	16.4	1.5	36	6	AR067934	AR067934 Sequence	C 295	16.2	1.5	40	6	I20146	I20146 Sequence
C 223	16.4	1.5	36	6	AR105323	AR105323 Sequence	C 296	16.2	1.5	41	6	A51237	A51237 Sequence
C 224	16.4	1.5	36	6	AR110680	AR110680 Sequence	C 297	16.2	1.5	41	6	AR112692	AR112692 Sequence
C 225	16.4	1.5	36	6	AR166793	AR166793 Sequence	C 298	16.2	1.5	41	6	AR113320	AR113320 Sequence
C 226	16.4	1.5	36	6	AX337941	AX337941 Sequence	C 299	16.2	1.5	41	6	AR134772	AR134772 Sequence
C 227	16.4	1.5	36	6	BD009957	BD009957 Sequence	C 300	16.2	1.5	41	6	AX107462	AX107462 Sequence
C 228	16.4	1.5	38	6	AR007229	AR007229 Sequence	C 301	16.2	1.5	42	6	A05097	A05097 Sequence
C 229	16.4	1.5	38	6	AR007230	AR007230 Sequence	C 302	16.2	1.5	43	6	AR136686	AR136686 Sequence
C 230	16.4	1.5	38	6	AR062433	AR062433 Sequence	C 303	16.2	1.5	43	6	AX078100	AX078100 Sequence
C 231	16.4	1.5	38	6	AR062434	AR062434 Sequence	C 304	16.2	1.5	44	6	A06666	A06666 Sequence
C 232	16.4	1.5	38	6	AR170015	AR170015 Sequence	C 305	16.2	1.5	44	6	AS8601	AS8601 Sequence
C 233	16.4	1.5	38	6	AR170016	AR170016 Sequence	C 306	16.2	1.5	44	6	AR049103	AR049103 Sequence
C 234	16.4	1.5	38	6	AR170442	AR170442 Sequence	C 307	16.2	1.5	44	6	AR161392	AR161392 Sequence
C 235	16.4	1.5	38	6	AR170443	AR170443 Sequence	C 308	16.2	1.5	44	6	E12782	E12782 DNA probe f
C 236	16.4	1.5	38	6	AX108295	AX108295 Sequence	C 309	16.2	1.5	45	6	A03928	A03928 Nucleotide
C 237	16.4	1.5	38	6	AX108397	AX108397 Sequence	C 310	16.2	1.5	45	6	A93937	A93937 Sequence
C 238	16.4	1.5	38	6	AX219671	AX219671 Sequence	C 311	16.2	1.5	45	6	AR16461	AR16461 Sequence
C 239	16.4	1.5	38	6	AX219696	AX219696 Sequence	C 312	16.2	1.5	45	6	AX046226	AX046226 Sequence
C 240	16.4	1.5	38	6	AX222866	AX222866 Sequence	C 313	16.2	1.5	45	6	AX046232	AX046232 Sequence
C 241	16.4	1.5	38	6	AX222881	AX222881 Sequence	C 314	16.2	1.5	45	6	AX046233	AX046233 Sequence
C 242	16.4	1.5	38	6	I06320	I06320 Sequence	C 315	16.2	1.5	45	6	AX046234	AX046234 Sequence
C 243	16.4	1.5	38	6	I27719	I27719 Sequence	C 316	16.2	1.5	45	10	MMU040692	MMU040692
C 244	16.4	1.5	38	6	I27720	I27720 Sequence	C 317	16.2	1.5	46	6	AR051079	AR051079 Sequence
C 245	16.4	1.5	39	6	A36987	A36987 Sequence	C 318	16.2	1.5	46	6	AX085867	AX085867 Sequence
C 246	16.4	1.5	39	6	A39195	A39195 Sequence	C 319	16.2	1.5	47	6	AX114375	AX114375 Sequence
C 247	16.4	1.5	39	6	A39254	A39254 Sequence	C 320	16.2	1.5	48	6	AX202561	AX202561 Sequence
C 248	16.4	1.5	39	6	AX134391	AX134391 Sequence	C 321	16.2	1.5	48	6	AX317303	AX317303 Sequence
C 249	16.4	1.5	39	6	BD004708	BD004708 Sequence	C 322	16.2	1.5	49	6	A38563	A38563 Sequence
C 250	16.4	1.5	40	6	A22794	A22794 Sequence	C 323	16.2	1.5	49	6	AR146496	AR146496 Sequence
C 251	16.4	1.5	40	6	AR031221	AR031221 Sequence	C 324	16.2	1.5	49	6	AX100863	AX100863 Sequence
C 252	16.4	1.5	40	6	AR145037	AR145037 Sequence	C 325	16.2	1.5	50	1	STMTNISC	STMTNISC
C 253	16.4	1.5	40	6	AR153209	AR153209 Sequence	C 326	16.2	1.5	50	3	GIKAR6	GIKAR6
C 254	16.4	1.5	40	6	AR163283	AR163283 Sequence	C 327	16.2	1.5	50	6	AR032602	AR032602 Sequence
C 255	16.4	1.5	40	6	AR176949	AR176949 Sequence	C 328	16.2	1.5	50	6	AR094171	AR094171 Sequence
C 256	16.4	1.5	41	6	A25708	A25708 M1381-8F0RN	C 329	16.2	1.5	50	6	AR103015	AR103015 Sequence
C 257	16.4	1.5	41	6	AR051380	AR051380 Sequence	C 330	16.2	1.5	50	6	AR105289	AR105289 Sequence
C 258	16.4	1.5	41	6	AX327071	AX327071 Sequence	C 331	16.2	1.5	50	6	AR172769	AR172769 Sequence
C 259	16.4	1.5	42	6	AX300421	AX300421 Sequence	C 332	16.2	1.5	50	6	AX158188	AX158188 Sequence
C 260	16.4	1.5	44	6	AR118021	AR118021 Sequence	C 333	16.2	1.5	50	6	AX164905	AX164905 Sequence
C 261	16.4	1.5	45	6	A40304	A40304 Sequence	C 334	16.2	1.5	50	6	AX165796	AX165796 Sequence
C 262	16.4	1.5	45	6	A52163	A52163 Sequence	C 335	16.2	1.5	50	6	E06610	E06610 probe DNA
C 263	16.4	1.5	45	6	A52167	A52167 Sequence	C 336	16.2	1.5	50	6	I29342	I29342 Sequence
C 264	16.4	1.5	45	6	A78546	A78546 Sequence	C 337	16.2	1.5	50	6	I80856	I80856 Sequence
C 265	16.4	1.5	45	6	AR014282	AR014282 Sequence	C 338	16.2	1.5	50	6	I91016	I91016 Sequence
C 266	16.4	1.5	45	6	AR016287	AR016287 Sequence	C 339	16.2	1.5	50	9	AF057517	AF057517 Homo sapi
C 267	16.4	1.5	45	6	AR103037	AR103037 Sequence	C 340	16.2	1.5	25	6	AR026642	AR026642 Sequence
C 268	16.4	1.5	45	6	AX080806	AX080806 Sequence	C 341	16.2	1.5	25	6	AR031296	AR031296 Sequence
C 269	16.4	1.5	45	6	AX191434	AX191434 Sequence	C 342	16.2	1.5	26	6	AR090836	AR090836 Sequence
C 270	16.4	1.5	45	6	I60386	I60386 Sequence	C 343	16.2	1.5	26	6	AR090895	AR090895 Sequence
C 271	16.4	1.5	46	8	S57741	S57741 5S rRNA [As	C 344	16.2	1.5	27	6	AX118520	AX118520 Sequence
C 272	16.4	1.5	48	6	BD004183	BD004183 RNP deriv	C 345	16.2	1.5	30	6	AR112494	AR112494 Sequence
C 273	16.4	1.5	48	6	AR107411	AR107411 Sequence	C 346	16.2	1.5	30	6	AR125838	AR125838 Sequence
C 274	16.4	1.5	50	6	AX079899	AX079899 Sequence	C 347	16.2	1.5	30	6	AX018472	AX018472 Sequence
C 275	16.2	1.5	22	6	AX079899	AX079899 Sequence	C 348	16.2	1.5	30	6	AX300428	AX300428 Sequence
C 276	16.2	1.5	27	6	E40016	E40016 Drug contai	C 349	16.2	1.5	30	6	E34429	E34429
C 277	16.2	1.5	29	6	E40824	E40824 Humanized a	C 350	16.2	1.5	30	6	I47250	I47250
C 278	16.2	1.5	29	6	E43370	E43370 Humanized a	C 351	16.2	1.5	30	6	I72720	I72720 Sequence
C 279	16.2	1.5	29	6	E43370	E43370 Humanized a	C 352	16.2	1.5	31	6	BD002849	BD002849 Gene comp
C 280	16.2	1.5	30	6	AR18255	AR18255 Sequence	C 353	16.2	1.5	34	6	A68999	A68999 Sequence
C 281	16.2	1.5	30	6	AR138658	AR138658 Sequence	C 354	16.2	1.5	34	6	AR139225	AR139225 Sequence
C 282	16.2	1.5	30	6	AX105564	AX105564 Sequence	C 355	16.2	1.5	35	6	AX201068	AX201068 Sequence
C 283	16.2	1.5	30	6	E64740	E64740 Method for	C 356	16.2	1.5	35	6	AX267867	AX267867 Sequence
C 284	16.2	1.5	31	6	AX249230	AX249230 Sequence	C 357	16.2	1.5	35	6	I56117	I56117 Sequence
C 285	16.2	1.5	33	6	AR084099	AR084099 Sequence	C 358	16.2	1.5	36	6	AX180183	AX180183 Sequence
C 286	16.2	1.5	34	6	AR045238	AR045238 Sequence	C 359	16.2	1.5	36	6	AX180683	AX180683 Sequence
C 287	16.2	1.5	34	6	I52290	I52290 Sequence	C 360	16.2	1.5	36	6	AX280204	AX280204 Sequence
C 288	16.2	1.5	36	6	AR131982	AR131982 Sequence	C 361	16.2	1.5	36	6	I39198	I39198
C 289	16.2	1.5	36	6	AR148746	AR148746 Sequence	C 362	16.2	1.5	36	6	I39507	I39507 Sequence
C 290	16.2	1.5	38	6	AX228131	AX228131 Sequence	C 363	16.2	1.5	36	6	I39545	I39545 Sequence
C 291	16.2	1.5	38	6	AX273564	AX273564 Sequence	C 364	16.2	1.5	36	6	I39546	I39546 Sequence
C 292	16.2	1.5	39	6	AX002153	AX002153 Sequence	C 365	16.2	1.5	37	6	AR089946	AR089946 Sequence

366	16	1.5	37	6	BD004797	BD004797 Novel pol	C 439	15.8	1.5	31	6	AR079830	AR079830 Sequence
367	16	1.5	37	6	I27101	I27101 Sequence 17	C 440	15.8	1.5	33	6	A23023	A23023 oligonucleo
368	16	1.5	37	6	I76318	I76318 Sequence 10	C 441	15.8	1.5	33	6	A64417	A64417 Sequence 30
369	16	1.5	37	23	E09672	E09672 PCR primer.	C 442	15.8	1.5	33	6	A99269	A99269 Sequence 45
370	16	1.5	38	6	AR141593	AR141593 Sequence	C 443	15.8	1.5	33	6	AR016274	AR016274 Sequence
371	16	1.5	38	6	AX218765	AX218765 Sequence	C 444	15.8	1.5	33	6	AR146987	AR146987 Sequence
372	16	1.5	38	6	BD001890	BD001890 Lumazine	C 445	15.8	1.5	33	6	AX172816	AX172816 Sequence
373	16	1.5	38	6	158761	158761 Sequence 26	C 446	15.8	1.5	33	6	I23841	I23841 Sequence 5
374	16	1.5	39	6	AR020690	AR020690 Sequence	C 447	15.8	1.5	34	6	AX137292	AX137292 Sequence
375	16	1.5	39	6	AR160282	AR160282 Sequence	C 448	15.8	1.5	34	6	E40006	E40006 drug contai
376	16	1.5	39	6	AX230529	AX230529 Sequence	C 449	15.8	1.5	34	6	E40814	E40814 Humanized a
377	16	1.5	40	6	AR169550	AR169550 Sequence	C 450	15.8	1.5	34	6	E43360	E43360 Humanized a
378	16	1.5	40	6	AX167630	AX167630 Sequence	C 451	15.8	1.5	35	6	AR008507	AR008507 Sequence
379	16	1.5	40	6	HPB1WT13R	HPB1WT13R Sequence	C 452	15.8	1.5	35	6	AX047077	AX047077 Sequence
380	16	1.5	42	6	AR104423	AR104423 Sequence	C 453	15.8	1.5	35	6	I12967	I12967 Sequence 26
381	16	1.5	42	6	AX287626	AX287626 Sequence	C 454	15.8	1.5	35	6	I15533	I15533 Sequence 12
382	16	1.5	42	6	AX287802	AX287802 Sequence	C 455	15.8	1.5	35	6	I16677	I16677 Sequence 17
383	16	1.5	43	6	A01530	A01530 Partial pro	C 456	15.8	1.5	35	6	I89430	I89430 Sequence 17
384	16	1.5	45	6	AB3672	AB3672 Sequence 15	C 457	15.8	1.5	36	6	A01938	A01938 Sequence 17
385	16	1.5	45	6	AR137560	AR137560 Sequence	C 458	15.8	1.5	36	6	A01939	A01939 N.meningitl1
386	16	1.5	45	6	AR139066	AR139066 Sequence	C 459	15.8	1.5	36	6	A64974	A64974 Sequence 4
387	16	1.5	45	6	AX214211	AX214211 Sequence	C 460	15.8	1.5	36	6	AR132538	AR132538 Sequence
388	16	1.5	45	10	MMTCSA2R2	X70725 M.musculus	C 461	15.8	1.5	36	6	BD004260	BD004260 Method fo
389	16	1.5	45	10	MMTCSA4B	X70726 M.musculus	C 462	15.8	1.5	36	6	E26546	E26546 DTMT gene
390	16	1.5	45	10	MMTCSA63	X70713 M.musculus	C 463	15.8	1.5	36	6	A59339	A59339 Sequence 11
391	16	1.5	45	10	MMTCSA1C7	AR006744 Sequence	C 464	15.8	1.5	37	6	AR045526	AR045526 Sequence
392	16	1.5	46	6	AR06744	AR032020 Sequence	C 465	15.8	1.5	38	6	AR046549	AR046549 Sequence
393	16	1.5	46	6	AR032020	AR038516 Sequence	C 466	15.8	1.5	38	6	AR165980	AR165980 Sequence
394	16	1.5	46	6	AR038516	AR050863 Sequence	C 467	15.8	1.5	38	6	AX000887	AX000887 Sequence
395	16	1.5	46	6	AR050863	AX085879 Sequence	C 468	15.8	1.5	38	6	AX133522	AX133522 Sequence
396	16	1.5	46	6	AX085879	E05889 Linker . 9/1	C 469	15.8	1.5	38	6	AX218548	AX218548 Sequence
397	16	1.5	46	6	E05889	E07920 Synthetic D	C 470	15.8	1.5	38	6	AX218856	AX218856 Sequence
398	16	1.5	46	6	E07920	A10487 oligonucleo	C 471	15.8	1.5	38	6	AX218984	AX218984 Sequence
399	16	1.5	47	6	A10487	A1645 oligonucleo	C 472	15.8	1.5	38	6	AX219421	AX219421 Sequence
400	16	1.5	47	6	AR13645	AR085283 Sequence	C 473	15.8	1.5	38	6	AX219592	AX219592 Sequence
401	16	1.5	47	6	AR085283	AX088325 Sequence	C 474	15.8	1.5	38	6	AX222479	AX222479 Sequence
402	16	1.5	47	6	AX088325	I17714 Sequence 14	C 475	15.8	1.5	38	6	AX228019	AX228019 Sequence
403	16	1.5	47	6	I17714	I18626 Sequence 14	C 476	15.8	1.5	38	6	AX228335	AX228335 Sequence
404	16	1.5	47	6	I18626	AR119465 Sequence	C 477	15.8	1.5	38	6	AX223687	AX223687 Sequence
405	16	1.5	48	6	AR119465	AR119466 Sequence	C 478	15.8	1.5	38	6	E60092	E60092 Endonucleas
406	16	1.5	48	6	AR119466	AR170400 Sequence	C 479	15.8	1.5	38	6	AX273780	AX273780 Sequence
407	16	1.5	48	6	AR170400	E59802 Polypeptide	C 480	15.8	1.5	38	6	AX273780	AX273780 Sequence
408	16	1.5	48	6	E59802	S67468 ND1...ND5 f	C 481	15.8	1.5	38	6	E60092	E60092 Endonucleas
409	16	1.5	48	9	S67468	E03641 Synthetic D	C 482	15.8	1.5	39	6	AX207915	AX207915 Sequence
410	16	1.5	49	6	E03641	A42872 Sequence 4	C 483	15.8	1.5	40	6	A33265	A33265 Synthetic I
411	16	1.5	50	6	A42872	AR027397 Sequence	C 484	15.8	1.5	40	6	AR148760	AR148760 Sequence
412	16	1.5	50	6	AR027397	AR027400 Sequence	C 485	15.8	1.5	40	6	AR148799	AR148799 Sequence
413	16	1.5	50	6	AR027400	AR028851 Sequence	C 486	15.8	1.5	41	6	AR109082	AR109082 Sequence
414	16	1.5	50	6	AR028851	AR028854 Sequence	C 487	15.8	1.5	41	6	AX327065	AX327065 Sequence
415	16	1.5	50	6	AR028854	AR032843 Sequence	C 488	15.8	1.5	42	6	A79143	A79143 Sequence 5
416	16	1.5	50	6	AR032843	AR034388 Sequence	C 489	15.8	1.5	42	6	AR174979	AR174979 Sequence
417	16	1.5	50	6	AR034388	AX157120 Sequence	C 490	15.8	1.5	42	6	AX207935	AX207935 Sequence
418	16	1.5	50	6	AR034391	AX160888 Sequence	C 491	15.8	1.5	42	6	BD007024	BD007024 Thermosta
419	16	1.5	50	6	AX157120	AX161340 Sequence	C 492	15.8	1.5	42	6	E25733	E25733 Method for
420	16	1.5	50	6	AX160888	AX162064 Sequence	C 493	15.8	1.5	43	6	AR174283	AR174283 Sequence
421	16	1.5	50	6	AX161340	AX165795 Sequence	C 494	15.8	1.5	43	6	A66382	A66382 Sequence 30
422	16	1.5	50	6	AX162064	E00658 Part of DNA	C 495	15.8	1.5	43	6	A03939	A03939 Nucleotide
423	16	1.5	50	6	AX165795	E00658 Part of DNA	C 496	15.8	1.5	45	6	AR112999	AR112999 Sequence
424	16	1.5	50	6	E00658	I29583 Sequence 45	C 497	15.8	1.5	45	6	AR163658	AR163658 Sequence
425	16	1.5	50	6	I29583	I43003 Sequence 25	C 498	15.8	1.5	45	6	AX259564	AX259564 Sequence
426	16	1.5	50	6	I43003	I52178 Sequence 1	C 499	15.8	1.5	45	6	HSTRK65	HSTRK65 H.sapiens m
427	16	1.5	50	6	I52178	I91257 Sequence 45	C 500	15.8	1.5	45	9	HSTRK7	HSTRK7 H.sapiens m
428	16	1.5	50	6	I91257	AR109737 Sequence	C 501	15.8	1.5	46	6	AR033925	AR033925 Sequence
429	16	1.5	50	6	AR109737	AX083943 Sequence	C 502	15.8	1.5	46	6	AR043084	AR043084 Sequence
430	15.8	1.5	28	6	AX083943	AX073734 Sequence	C 503	15.8	1.5	46	6	AR161342	AR161342 Sequence
431	15.8	1.5	29	6	AX073734	AX067967 Sequence	C 504	15.8	1.5	46	6	AR175058	AR175058 Sequence
432	15.8	1.5	29	6	AX067967	AR003363 Sequence	C 505	15.8	1.5	46	6	AX032490	AX032490 Sequence
433	15.8	1.5	30	6	AR003363	AR027435 Sequence	C 506	15.8	1.5	46	6	AX207947	AX207947 Sequence
434	15.8	1.5	30	6	AR027435	AR028215 Sequence	C 507	15.8	1.5	47	6	AR011525	AR011525 Sequence
435	15.8	1.5	30	6	AR028215	AR067867 Sequence	C 508	15.8	1.5	47	6	AR032537	AR032537 Sequence
436	15.8	1.5	30	6	AR067867	AR186618 Sequence	C 509	15.8	1.5	47	6	AX085321	AX085321 Sequence
437	15.8	1.5	30	6	AR186618	I85539 Sequence 5	C 510	15.8	1.5	47	6	AX114349	AX114349 Sequence
438	15.8	1.5	30	6	I85539		C 511	15.8	1.5	47	6	E40590	E40590 Novel prote

512	15.8	1.5	47	6	I18163	I18163 Sequence 40	585	15.6	1.4	32	6	174500	174500 Sequence 4
C 513	15.8	1.5	47	6	I29277	I29277 Sequence 14	C 586	15.6	1.4	33	6	AR137784	AR137784 Sequence
514	15.8	1.5	47	6	I90951	I90951 Sequence 14	587	15.6	1.4	33	9	HS249321	HS249321 Homo sapi
515	15.8	1.5	48	6	AR075818	AR075818 Sequence	588	15.6	1.4	33	9	HUMMB3506	M28114 Human MHC c
516	15.8	1.5	48	6	AR098735	AR098735 Sequence	589	15.6	1.4	33	9	HUMMB3506	M22791 Human MHC c
517	15.8	1.5	48	6	AX076554	AX076554 Sequence	590	15.6	1.4	33	9	HUMMB3506	M22791 Human MHC c
518	15.8	1.5	48	6	E30451	E30451 Method for	C 591	15.6	1.4	34	6	AR024035	AR024035 Sequence
519	15.8	1.5	48	6	E35694	E35694 Detection a	C 592	15.6	1.4	34	6	AR024040	AR024040 Sequence
520	15.8	1.5	48	6	I26695	I26695 Sequence 11	C 593	15.6	1.4	34	6	BD004103	BD004103 Apoptosis
521	15.8	1.5	48	6	I82381	I82381 Sequence 11	C 594	15.6	1.4	34	6	BD005213	BD005213 Novel yea
522	15.8	1.5	48	6	I93725	I93725 Sequence 11	C 595	15.6	1.4	34	6	I21118	I21118 Sequence 3
C 523	15.8	1.5	48	9	HS014089	HS014089 Human cell	C 596	15.6	1.4	34	6	I59739	I59739 Sequence 3
C 524	15.8	1.5	48	9	HS014091	HS014091 Human cell	C 597	15.6	1.4	35	11	C75747	C75747 Homo sapien
525	15.8	1.5	48	10	AB001360	AB001360 Mus muscu	598	15.6	1.4	36	6	A18752	A18752 oligonucleo
C 526	15.8	1.5	49	6	A02567	A02567 Nucleotide	599	15.6	1.4	36	6	A59370	A59370 Sequence 20
C 527	15.8	1.5	49	6	A97641	A97641 Sequence 8	C 600	15.6	1.4	36	6	A59373	A59373 Sequence 23
528	15.8	1.5	49	6	AR076915	AR076915 Sequence	C 601	15.6	1.4	36	6	A78792	A78792 Sequence 13
529	15.8	1.5	49	6	AR167306	AR167306 Sequence	C 602	15.6	1.4	36	6	AR104371	AR104371 Sequence
530	15.8	1.5	49	6	I42245	I42245 Sequence 58	C 603	15.6	1.4	36	6	AR121370	AR121370 Sequence
531	15.8	1.5	50	6	AR040810	AR040810 Sequence	C 604	15.6	1.4	36	6	AR171382	AR171382 Sequence
C 532	15.8	1.5	50	6	AR151517	AR151517 Sequence	C 605	15.6	1.4	36	6	I12254	I12254 Sequence 23
533	15.8	1.5	50	6	AR151518	AR151518 Sequence	606	15.6	1.4	36	6	I17245	I17245 Sequence 13
534	15.8	1.5	50	6	AR151520	AR151520 Sequence	607	15.6	1.4	36	6	I58776	I58776 Sequence 23
535	15.8	1.5	50	6	AR151521	AR151521 Sequence	C 608	15.6	1.4	37	6	AR069344	AR069344 Sequence
C 536	15.8	1.5	50	6	AR155994	AR155994 Sequence	C 609	15.6	1.4	37	6	AX228565	AX228565 Sequence
537	15.8	1.5	50	6	AX164811	AX164811 Sequence	C 610	15.6	1.4	37	6	I64561	I64561 Sequence 9
C 538	15.8	1.5	50	6	AX175389	AX175389 Sequence	C 611	15.6	1.4	38	6	AR047223	AR047223 Sequence
C 539	15.8	1.5	50	6	I28909	I28909 Sequence 7	C 612	15.6	1.4	38	6	AR071010	AR071010 Sequence
540	15.8	1.5	50	6	I28910	I28910 Sequence 8	C 613	15.6	1.4	38	6	I37753	I37753 Sequence 76
541	15.8	1.5	50	6	I72317	I72317 Sequence 26	C 614	15.6	1.4	38	6	I54275	I54275 Sequence 20
542	15.8	1.5	50	6	I79574	I79574 Sequence 19	C 615	15.6	1.4	38	6	I94603	I94603 Sequence 76
543	15.8	1.5	50	9	CEBSAT2	CEBSAT2	C 616	15.6	1.4	39	6	A63057	A63057 Sequence 1
544	15.6	1.4	22	6	AR031295	AR031295 Sequence	C 617	15.6	1.4	39	6	AR050321	AR050321 Sequence
545	15.6	1.4	23	6	E05223	E05223 Primer for	C 618	15.6	1.4	39	6	AR111718	AR111718 Sequence
546	15.6	1.4	23	6	E16506	E16506 PCR primer	C 619	15.6	1.4	39	6	AX057328	AX057328 Sequence
C 547	15.6	1.4	24	6	AX289704	AX289704 Sequence	620	15.6	1.4	40	6	AR111427	AR111427 Sequence
548	15.6	1.4	24	6	AX290808	AX290808 Sequence	621	15.6	1.4	40	6	AR163284	AR163284 Sequence
549	15.6	1.4	24	6	E08145	E08145 PCR primer	622	15.6	1.4	40	6	AR176950	AR176950 Sequence
C 550	15.6	1.4	25	6	AX197334	AX197334 Sequence	623	15.6	1.4	40	6	AX176950	AX176950 Sequence
C 551	15.6	1.4	25	6	AX197336	AX197336 Sequence	624	15.6	1.4	40	6	AX176950	AX176950 Sequence
552	15.6	1.4	25	6	E34111	E34111 Protein par	C 625	15.6	1.4	40	6	AX156927	AX156927 Sequence
C 553	15.6	1.4	27	6	I69008	I69008 Sequence 27	C 626	15.6	1.4	40	6	AX156927	AX156927 Sequence
554	15.6	1.4	28	9	HS278047	HS278047 H.sapiens T	C 627	15.6	1.4	41	6	AX107448	AX107448 Sequence
555	15.6	1.4	29	6	E08130	E08130 DNA encodin	C 628	15.6	1.4	41	6	AX107448	AX107448 Sequence
C 556	15.6	1.4	30	6	A48363	A48363 Sequence 8	629	15.6	1.4	41	6	AX180260	AX180260 Sequence
C 557	15.6	1.4	30	6	AR122007	AR122007 Sequence	630	15.6	1.4	42	6	A11159	A11159 synthetic o
558	15.6	1.4	31	6	AX304840	AX304840 Sequence	631	15.6	1.4	42	6	A20310	A20310 Neo 6 oligo
559	15.6	1.4	31	6	AR076838	AR076838 Sequence	C 632	15.6	1.4	42	6	AX107219	AX107219 Sequence
560	15.6	1.4	31	6	AR088995	AR088995 Sequence	C 633	15.6	1.4	42	6	BD010097	BD010097 Cyclic de
561	15.6	1.4	31	6	AR172659	AR172659 Sequence	C 634	15.6	1.4	42	6	E00785	E00785 MOX-NEOR ge
562	15.6	1.4	31	6	AX006885	AX006885 Sequence	C 635	15.6	1.4	43	6	AX107466	AX107466 Sequence
C 563	15.6	1.4	31	6	AX248254	AX248254 Sequence	636	15.6	1.4	43	6	AX107466	AX107466 Sequence
C 564	15.6	1.4	31	6	AX280715	AX280715 Sequence	C 637	15.6	1.4	43	6	E23361	E23361 Virus vecto
565	15.6	1.4	31	6	AX280716	AX280716 Sequence	638	15.6	1.4	43	6	AX201011	AX201011 Sequence
C 566	15.6	1.4	31	6	I21134	I21134 Sequence 19	639	15.6	1.4	45	6	AX267810	AX267810 Sequence
C 567	15.6	1.4	31	6	I59755	I59755 Sequence 19	C 640	15.6	1.4	45	6	HS242434	HS242434 Homo sapi
568	15.6	1.4	31	6	I74794	I74794 Sequence 10	C 641	15.6	1.4	46	6	AX040127	AX040127 Sequence
C 569	15.6	1.4	32	6	AR001358	AR001358 Sequence	C 642	15.6	1.4	46	6	AX076702	AX076702 Sequence
C 570	15.6	1.4	32	6	AR044843	AR044843 Sequence	C 643	15.6	1.4	46	6	AX076702	AX076702 Sequence
C 571	15.6	1.4	32	6	AR044853	AR044853 Sequence	644	15.6	1.4	46	6	AX020144	AX020144 Sequence
C 572	15.6	1.4	32	6	AR052229	AR052229 Sequence	645	15.6	1.4	47	6	AR040808	AR040808 Sequence
C 573	15.6	1.4	32	6	AR052239	AR052239 Sequence	646	15.6	1.4	47	6	AR050331	AR050331 Sequence
C 574	15.6	1.4	32	6	AR078338	AR078338 Sequence	647	15.6	1.4	47	6	AX194695	AX194695 Sequence
C 575	15.6	1.4	32	6	AR085189	AR085189 Sequence	648	15.6	1.4	47	6	AX201573	AX201573 Sequence
C 576	15.6	1.4	32	6	AR138109	AR138109 Sequence	C 649	15.6	1.4	48	6	AR142488	AR142488 Sequence
577	15.6	1.4	32	6	AX281027	AX281027 Sequence	C 650	15.6	1.4	48	6	AX147895	AX147895 Sequence
578	15.6	1.4	32	6	E06329	E06329 Primer 9/1	C 651	15.6	1.4	48	6	AX147924	AX147924 Sequence
579	15.6	1.4	32	6	E06525	E06525 Primer 9/1	C 652	15.6	1.4	48	6	HS240389	HS240389 Homo sapi
580	15.6	1.4	32	6	E59198	E59198 Method for	C 653	15.6	1.4	49	6	AX260258	AX260258 Sequence
581	15.6	1.4	32	6	E64379	E64379 Process of	C 654	15.6	1.4	49	6	AX279613	AX279613 Sequence
C 582	15.6	1.4	32	6	I28179	I28179 Sequence 22	C 655	15.6	1.4	50	6	AR032714	AR032714 Sequence
C 583	15.6	1.4	32	6	I33893	I33893 Sequence 1	656	15.6	1.4	50	6	AR032945	AR032945 Sequence
C 584	15.6	1.4	32	6	I33903	I33903 Sequence 11	C 657	15.6	1.4	50	6	AR120971	AR120971 Sequence

658	15.6	1.4	50	6	AX074249	AX074249 Sequence	731	15.4	1.4	37	6	AX220058	AX220058 Sequence
659	15.6	1.4	50	6	AX157400	AX157400 Sequence	732	15.4	1.4	37	6	AX220100	AX220100 Sequence
660	15.6	1.4	50	6	AX158834	AX158834 Sequence	733	15.4	1.4	37	10	MUSBMP2AD	AX220100 Mouse gene
661	15.6	1.4	50	6	AX160890	AX160890 Sequence	734	15.4	1.4	38	6	A44448	A44448 Sequence
662	15.6	1.4	50	6	AX161884	AX161884 Sequence	735	15.4	1.4	38	6	AR009693	AR009693 Sequence
663	15.6	1.4	50	6	AX162041	AX162041 Sequence	736	15.4	1.4	38	6	AR058094	AR058094 Sequence
664	15.6	1.4	50	6	AX327735	AX327735 Sequence	737	15.4	1.4	38	6	AR115852	AR115852 Sequence
665	15.6	1.4	50	6	AX327810	AX327810 Sequence	738	15.4	1.4	38	6	AX218802	AX218802 Sequence
666	15.6	1.4	50	6	AX338568	AX338568 Sequence	739	15.4	1.4	38	6	AX219623	AX219623 Sequence
667	15.6	1.4	50	6	129454	129454 Sequence	740	15.4	1.4	38	6	AX220379	AX220379 Sequence
668	15.6	1.4	50	6	129685	129685 Sequence	741	15.4	1.4	38	6	AX222558	AX222558 Sequence
669	15.6	1.4	50	6	142254	142254 Sequence	742	15.4	1.4	38	6	AX222692	AX222692 Sequence
670	15.6	1.4	50	6	142265	142265 Sequence	743	15.4	1.4	38	6	AX222783	AX222783 Sequence
671	15.6	1.4	50	6	191128	191128 Sequence	744	15.4	1.4	38	6	AX222827	AX222827 Sequence
672	15.6	1.4	50	6	191359	191359 Sequence	745	15.4	1.4	38	6	AX222845	AX222845 Sequence
673	15.6	1.4	50	9	HSEDA05	AF060781 Homo sapi	746	15.4	1.4	38	6	AX222942	AX222942 Sequence
674	15.4	1.4	21	6	AX095763	AX095763 Sequence	747	15.4	1.4	38	6	AX227929	AX227929 Sequence
675	15.4	1.4	25	6	AR003620	AR003620 Sequence	748	15.4	1.4	38	6	AX228045	AX228045 Sequence
676	15.4	1.4	25	6	AR030482	AR030482 Sequence	749	15.4	1.4	38	6	AX273367	AX273367 Sequence
677	15.4	1.4	25	6	AR030484	AR030484 Sequence	750	15.4	1.4	38	6	A62086	A62086 Sequence
678	15.4	1.4	25	6	AX115508	AX115508 Sequence	751	15.4	1.4	39	6	A66029	A66029 Sequence
679	15.4	1.4	25	6	AX321448	AX321448 Sequence	752	15.4	1.4	39	6	AR022077	AR022077 Sequence
680	15.4	1.4	25	6	117003	117003 Sequence	753	15.4	1.4	39	6	AR088022	AR088022 Sequence
681	15.4	1.4	27	6	AR060294	AR060294 Sequence	754	15.4	1.4	39	6	AR11877	AR11877 Sequence
682	15.4	1.4	27	6	AR130222	AR130222 Sequence	755	15.4	1.4	39	6	AR154819	AR154819 Sequence
683	15.4	1.4	27	6	AX138048	AX138048 Sequence	756	15.4	1.4	39	6	AX008137	AX008137 Sequence
684	15.4	1.4	27	6	E31817	E31817 Method for	757	15.4	1.4	39	6	AX008138	AX008138 Sequence
685	15.4	1.4	27	6	120954	120954 Sequence	758	15.4	1.4	39	6	AX097527	AX097527 Sequence
686	15.4	1.4	28	6	AR090184	AR090184 Sequence	759	15.4	1.4	39	6	192867	192867 Sequence
687	15.4	1.4	28	6	AR082930	AR082930 Sequence	760	15.4	1.4	40	6	A35759	A35759 Sequence
688	15.4	1.4	29	6	AR048868	AR048868 Sequence	761	15.4	1.4	40	6	A41990	A41990 Sequence
689	15.4	1.4	29	6	AX027242	AX027242 Sequence	762	15.4	1.4	40	6	AR076923	AR076923 Sequence
690	15.4	1.4	30	6	A46144	BD011249 Human tel	763	15.4	1.4	40	6	AR078313	AR078313 Sequence
691	15.4	1.4	30	6	BD011249	BD011249 Human telom	764	15.4	1.4	40	6	AR085416	AR085416 Sequence
692	15.4	1.4	30	6	E36998	E36998 Human telom	765	15.4	1.4	40	6	AR103372	AR103372 Sequence
693	15.4	1.4	31	6	137176	137176 Sequence	766	15.4	1.4	40	6	AR135232	AR135232 Sequence
694	15.4	1.4	31	6	194026	194026 Sequence	767	15.4	1.4	40	6	AR146728	AR146728 Sequence
695	15.4	1.4	32	6	AR090309	AR090309 Sequence	768	15.4	1.4	40	6	AR152299	AR152299 Sequence
696	15.4	1.4	33	6	A71570	A71570 Sequence	769	15.4	1.4	40	6	AR157837	AR157837 Sequence
697	15.4	1.4	33	6	A93834	A93834 Sequence	770	15.4	1.4	40	6	AR169007	AR169007 Sequence
698	15.4	1.4	33	6	AX000220	AX000220 Sequence	771	15.4	1.4	40	6	AR169229	AR169229 Sequence
699	15.4	1.4	33	6	AX017174	AX017174 Sequence	772	15.4	1.4	40	6	104917	104917 Sequence
700	15.4	1.4	33	6	BD008563	BD008563 Antifunga	773	15.4	1.4	41	6	AR107042	AR107042 Sequence
701	15.4	1.4	33	9	S79313	S79313 hprt-hypoxa	774	15.4	1.4	41	6	A09949	A09949 Sequence
702	15.4	1.4	33	23	E10544	E10544 PCR primer	775	15.4	1.4	42	6	A11529	A11529 Sequence
703	15.4	1.4	34	6	A84472	A84472 Sequence	776	15.4	1.4	42	6	A76875	A76875 Sequence
704	15.4	1.4	34	6	AX343105	AX343105 Sequence	777	15.4	1.4	42	6	AR031987	AR031987 Sequence
705	15.4	1.4	35	6	A79778	A79778 Sequence	778	15.4	1.4	42	6	AR049353	AR049353 Sequence
706	15.4	1.4	35	6	AR006748	AR006748 Sequence	779	15.4	1.4	42	6	AR168292	AR168292 Sequence
707	15.4	1.4	35	6	AR018108	AR018108 Sequence	780	15.4	1.4	42	6	AR173587	AR173587 Sequence
708	15.4	1.4	35	6	AR032024	AR032024 Sequence	781	15.4	1.4	42	6	AR173587	AR173587 Sequence
709	15.4	1.4	35	6	AR038520	AR038520 Sequence	782	15.4	1.4	42	10	MM0232727	MM0232727 Sequence
710	15.4	1.4	35	6	AR050867	AR050867 Sequence	783	15.4	1.4	43	6	AR019544	AR019544 Sequence
711	15.4	1.4	35	6	AR144795	AR144795 Sequence	784	15.4	1.4	43	6	AR100959	AR100959 Sequence
712	15.4	1.4	35	6	AX232234	AX232234 Sequence	785	15.4	1.4	43	6	AR108505	AR108505 Sequence
713	15.4	1.4	35	6	E05891	E05891 Linker. 9/1	786	15.4	1.4	43	6	AR138396	AR138396 Sequence
714	15.4	1.4	35	6	E07924	E07924 Synthetic D	787	15.4	1.4	43	6	AX107459	AX107459 Sequence
715	15.4	1.4	35	6	108942	108942 Sequence	788	15.4	1.4	43	6	155676	155676 Sequence
716	15.4	1.4	35	6	HDM3E12M5	D17038 Human HepG2	789	15.4	1.4	43	6	176453	176453 Sequence
717	15.4	1.4	35	9	AR041491	AR041491 Sequence	790	15.4	1.4	44	6	GGU62254	GGU62254 Sequence
718	15.4	1.4	36	6	AR041564	AR041564 Sequence	791	15.4	1.4	44	6	A13587	A13587 Sequence
719	15.4	1.4	36	6	AR041998	AR041998 Sequence	792	15.4	1.4	44	6	A13594	A13594 Sequence
720	15.4	1.4	36	6	AR042089	AR042089 Sequence	793	15.4	1.4	44	6	AR161381	AR161381 Sequence
721	15.4	1.4	36	6	AR132477	AR132477 Sequence	794	15.4	1.4	44	6	S79613S1	S79613S1 Sequence
722	15.4	1.4	36	6	AR132478	AR132478 Sequence	795	15.4	1.4	44	6	AB022054	AB022054 Sequence
723	15.4	1.4	36	6	AR132479	AR132479 Sequence	796	15.4	1.4	45	6	A05114	A05114 Sequence
724	15.4	1.4	36	6	AX127923	AX127923 Sequence	797	15.4	1.4	45	6	AR00025	AR00025 Sequence
725	15.4	1.4	36	6	AX134762	AX134762 Sequence	798	15.4	1.4	45	6	AR33229	AR33229 Sequence
726	15.4	1.4	37	6	A59249	A59249 Sequence	799	15.4	1.4	45	6	AR163658	AR163658 Sequence
727	15.4	1.4	37	6	A68997	A68997 Sequence	800	15.4	1.4	45	6	AR163658	AR163658 Sequence
728	15.4	1.4	37	6	A69057	A69057 Sequence	801	15.4	1.4	45	6	AX085871	AX085871 Sequence
729	15.4	1.4	37	6	AR139223	AR139223 Sequence	802	15.4	1.4	45	6	AX259564	AX259564 Sequence
730	15.4	1.4	37	6	AR150581	AR150581 Sequence	803	15.4	1.4	45	9	HSCD85708	HSCD85708 Sequence
													AX220058 Sequence
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													AX273367 Sequence
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													AX008138 Sequence
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													A41990 Sequence
													AR076923 Sequence
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													AR103372 Sequence
													AR135232 Sequence
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													AR107042 Sequence
											</		

C 804	15.4	1.4	45	9	HSU14050	U14050 Human T cel	877	15.2	1.4	30	6	AR104060	AR104060 Sequence
C 805	15.4	1.4	46	6	AR000193	AR000193 Sequence	C 878	15.2	1.4	30	6	AR175856	AR175856 Sequence
C 806	15.4	1.4	46	6	AR074551	AR074551 Sequence	C 879	15.2	1.4	30	6	AX000923	AX000923 Sequence
C 807	15.4	1.4	46	6	AR157431	AR157431 Sequence	C 880	15.2	1.4	30	6	AX256489	AX256489 Sequence
C 808	15.4	1.4	46	6	AX003472	AX003472 Sequence	C 881	15.2	1.4	30	6	125922	125922 Sequence 2
C 809	15.4	1.4	46	6	106580	106580 Sequence 6	C 882	15.2	1.4	30	6	AR038284	AR038284 Sequence
C 810	15.4	1.4	47	6	AR026608	AR026608 Sequence	C 883	15.2	1.4	31	6	AR147025	AR147025 Sequence
C 811	15.4	1.4	47	6	AR029106	AR029106 Sequence	C 884	15.2	1.4	31	6	AR152706	AR152706 Sequence
C 812	15.4	1.4	47	6	AR032492	AR032492 Sequence	C 885	15.2	1.4	31	6	AX151268	AX151268 Sequence
C 813	15.4	1.4	47	6	AR053345	AR053345 Sequence	C 886	15.2	1.4	31	6	AX248352	AX248352 Sequence
C 814	15.4	1.4	47	6	AX194963	AX194963 Sequence	C 887	15.2	1.4	31	6	AX249231	AX249231 Sequence
C 815	15.4	1.4	47	6	AX195036	AX195036 Sequence	C 888	15.2	1.4	31	6	AX249286	AX249286 Sequence
C 816	15.4	1.4	47	6	129232	129232 Sequence 10	C 889	15.2	1.4	31	6	AX233345	AX233345 Sequence
C 817	15.4	1.4	47	6	190906	190906 Sequence 10	C 890	15.2	1.4	31	6	161318	161318 Sequence 39
C 818	15.4	1.4	48	6	AX036818	AX036818 Sequence	C 891	15.2	1.4	31	6	A39292	A39292 Sequence 12
C 819	15.4	1.4	48	6	AX136891	AX136891 Sequence	C 892	15.2	1.4	31	6	124846	124846 Sequence 17
C 820	15.4	1.4	48	6	AX223609	AX223609 Sequence	C 893	15.2	1.4	32	6	172667	172667 Sequence 29
C 821	15.4	1.4	48	6	E40904	E40904 Humanized a	C 894	15.2	1.4	32	6	188873	188873 Sequence 7
C 822	15.4	1.4	48	6	HLVCDR3H	HLVCDR3H	C 895	15.2	1.4	32	6	AR136818	AR136818 Sequence
C 823	15.4	1.4	49	5	CIHADBDA	M24168 Duck alpha-	C 896	15.2	1.4	32	6	AR152527	AR152527 Sequence
C 824	15.4	1.4	49	5	AR017857	AR017857 Sequence	C 897	15.2	1.4	32	6	AR136818	AR136818 Sequence
C 825	15.4	1.4	49	5	AR065822	AR065822 Sequence	C 898	15.2	1.4	33	6	AR152527	AR152527 Sequence
C 826	15.4	1.4	49	6	AX046596	AX046596 Sequence	C 899	15.2	1.4	33	6	AX203806	AX203806 Sequence
C 827	15.4	1.4	49	6	E13211	E13211 PCR primer.	C 900	15.2	1.4	33	6	168140	168140 Sequence 8
C 828	15.4	1.4	49	6	106741	106741 Sequence 10	C 901	15.2	1.4	33	10	MMTG35M	MMTG35M Sequence 4
C 829	15.4	1.4	49	6	142246	142246 Sequence 59	C 902	15.2	1.4	34	6	A63532	A63532 Sequence 4
C 830	15.4	1.4	49	6	AR027352	AR027352 Sequence	C 903	15.2	1.4	34	6	AR122908	AR122908 Sequence 4
C 831	15.4	1.4	49	6	AR027405	AR027405 Sequence	C 904	15.2	1.4	34	6	148990	148990 Sequence 10
C 832	15.4	1.4	50	6	AR028806	AR028806 Sequence	C 905	15.2	1.4	34	6	152089	152089 Sequence 10
C 833	15.4	1.4	50	6	AR028859	AR028859 Sequence	C 906	15.2	1.4	34	6	170356	170356 Sequence 10
C 834	15.4	1.4	50	6	AR034343	AR034343 Sequence	C 907	15.2	1.4	34	6	186382	186382 Sequence 10
C 835	15.4	1.4	50	6	AR034396	AR034396 Sequence	C 908	15.2	1.4	34	6	A41034	A41034 Sequence 3
C 836	15.4	1.4	50	6	AX156816	AX156816 Sequence	C 909	15.2	1.4	35	6	AR061504	AR061504 Sequence
C 837	15.4	1.4	50	6	AX160890	AX160890 Sequence	C 910	15.2	1.4	35	6	AR108403	AR108403 Sequence
C 838	15.4	1.4	50	6	AX161202	AX161202 Sequence	C 911	15.2	1.4	35	6	108871	108871 Sequence 12
C 839	15.4	1.4	50	6	AX161676	AX161676 Sequence	C 912	15.2	1.4	35	6	116360	116360 Sequence 18
C 840	15.4	1.4	50	6	AX162966	AX162966 Sequence	C 913	15.2	1.4	35	6	166846	166846 Sequence 18
C 841	15.4	1.4	50	6	AX165091	AX165091 Sequence	C 914	15.2	1.4	35	6	181244	181244 Sequence 3
C 842	15.4	1.4	50	6	AX303593	AX303593 Sequence	C 915	15.2	1.4	35	6	184940	184940 Sequence 18
C 843	15.4	1.4	50	6	E16496	E16496 Pseudomonas	C 916	15.2	1.4	35	6	AR007301	AR007301 Sequence
C 844	15.4	1.4	50	6	107577	107577 Sequence 6	C 917	15.2	1.4	36	6	AR009853	AR009853 Sequence
C 845	15.4	1.4	50	6	S72295S4	S72295 Gria-Platel	C 918	15.2	1.4	36	6	AR036682	AR036682 Sequence
C 846	15.4	1.4	50	10	MMTFAM10	U71395 Mus musculus	C 919	15.2	1.4	36	6	AR028386	AR028386 Sequence
C 847	15.4	1.4	50	6	AR162376	AR162376 Sequence	C 920	15.2	1.4	36	6	AX028390	AX028390 Sequence
C 848	15.4	1.4	50	6	102470	102470 Sequence 2	C 921	15.2	1.4	36	6	AX280378	AX280378 Sequence
C 849	15.2	1.4	20	6	182334	182334 Sequence 7	C 922	15.2	1.4	36	6	E16102	E16102 PCR primer
C 850	15.2	1.4	20	6	117187	117187 Sequence 7	C 923	15.2	1.4	36	6	E63397	E63397 Inhibitory
C 851	15.2	1.4	21	6	SSA1788	AR0200788 Sus scrofa	C 924	15.2	1.4	36	6	E42373	E42373 Inhibitory
C 852	15.2	1.4	22	6	AR028443	AR028443 Sequence	C 925	15.2	1.4	36	6	177730	177730 Sequence 2
C 853	15.2	1.4	22	6	AR089965	AR089965 Sequence	C 926	15.2	1.4	36	6	177982	177982 Sequence 68
C 854	15.2	1.4	22	6	AX155247	AX155247 Sequence	C 927	15.2	1.4	36	6	AX26652	AX26652 Sequence 10
C 855	15.2	1.4	24	6	AX327692	AX327692 Sequence	C 928	15.2	1.4	36	6	AR093984	AR093984 Sequence
C 856	15.2	1.4	25	6	143286	143286 Sequence 10	C 929	15.2	1.4	37	6	AX027380	AX027380 Sequence
C 857	15.2	1.4	25	6	AR090663	AR090663 Sequence	C 930	15.2	1.4	37	6	AR046779	AR046779 Sequence
C 858	15.2	1.4	26	6	AL1158	AL1158 synthetic O	C 931	15.2	1.4	38	6	AR047181	AR047181 Sequence
C 859	15.2	1.4	28	6	E20309	E20309 Neo 3 Oligo	C 932	15.2	1.4	38	6	AR047567	AR047567 Sequence
C 860	15.2	1.4	28	6	E00784	E00784 MOX-NEOR ge	C 933	15.2	1.4	38	6	AR055721	AR055721 Sequence
C 861	15.2	1.4	28	6	AR089204	AR089204 Sequence	C 934	15.2	1.4	38	6	AR130066	AR130066 Sequence
C 862	15.2	1.4	29	6	AX008686	AX008686 Sequence	C 935	15.2	1.4	38	6	AR170046	AR170046 Sequence
C 863	15.2	1.4	29	6	AX179408	AX179408 Sequence	C 936	15.2	1.4	38	6	AR172683	AR172683 Sequence
C 864	15.2	1.4	29	6	A45995	A45995 Sequence 3	C 937	15.2	1.4	38	6	AR218902	AR218902 Sequence
C 865	15.2	1.4	29	6	A60619	A60619 Sequence 4	C 938	15.2	1.4	38	6	AX227916	AX227916 Sequence
C 866	15.2	1.4	30	6	A64562	A64562 Sequence 3	C 939	15.2	1.4	38	6	AX228036	AX228036 Sequence
C 867	15.2	1.4	30	6	A81419	A81419 Sequence 9	C 940	15.2	1.4	38	6		
C 868	15.2	1.4	30	6	A81475	A81475 Sequence 9	C 941	15.2	1.4	38	6		
C 869	15.2	1.4	30	6	A92605	A92605 Sequence 4	C 942	15.2	1.4	38	6		
C 870	15.2	1.4	30	6	A93787	A93787 Sequence 3	C 943	15.2	1.4	38	6		
C 871	15.2	1.4	30	6	AR104023	AR104023 Sequence	C 944	15.2	1.4	38	6		
C 872	15.2	1.4	30	6	AR104058	AR104058 Sequence	C 945	15.2	1.4	38	6		
C 873	15.2	1.4	30	6	AR104059	AR104059 Sequence	C 946	15.2	1.4	38	6		
C 874	15.2	1.4	30	6			C 947	15.2	1.4	38	6		
C 875	15.2	1.4	30	6			C 948	15.2	1.4	38	6		
C 876	15.2	1.4	30	6			C 949	15.2	1.4	38	6		

c 950 15.2 1.4 38 6 AX228473  
 c 951 15.2 1.4 38 6 AX273515  
 c 952 15.2 1.4 38 6 106985  
 c 953 15.2 1.4 38 6 153831  
 c 954 15.2 1.4 38 6 154233  
 c 955 15.2 1.4 38 6 154619  
 c 956 15.2 1.4 38 6 154835  
 c 957 15.2 1.4 39 6 A14917  
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 c 959 15.2 1.4 39 6 AR021430  
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 c 961 15.2 1.4 39 6 AR042992  
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 c 965 15.2 1.4 39 6 AR116325  
 c 966 15.2 1.4 39 6 AR161326  
 c 967 15.2 1.4 39 6 AX112900  
 c 968 15.2 1.4 39 6 AX194761  
 c 969 15.2 1.4 39 6 E59837  
 c 970 15.2 1.4 39 6 E59837  
 c 971 15.2 1.4 39 6 I43971  
 c 972 15.2 1.4 39 6 I43971  
 c 973 15.2 1.4 39 6 I62982  
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 c 999 15.2 1.4 39 6 I62982  
 c 1000 15.2 1.4 39 6 I62982

## ALIGNMENTS

RESULT 1  
 LOCUS AR021485 42 bp DNA linear PAT 05-DEC-1998  
 DEFINITION Sequence 13 from patent US 5789655.  
 ACCESSION AR021485  
 VERSION AR021485.1 GI:3976100  
 KEYWORDS  
 ORGANISM Unknown.  
 SOURCE Unknown.  
 REFERENCE  
 1 (bases 1 to 42)  
 Prusiner,S.B., Telling,G.C., Cohen,F.E. and Scott,M.R.  
 Transgenic animals expressing artificial epitope-tagged proteins  
 Patent: US 5789655-A 13 04-ADG-1998;  
 JOURNAL Location/Qualifiers  
 FEATURES  
 source 1..42  
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BASE COUNT 6 a 15 c 10 g 11 t  
 ORIGIN  
 Query Match 2.0%; Score 21.2; DB 6; Length 42;  
 Best Local Similarity 69.0%; Pred. No. 3.4e+05;  
 Matches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 540 CCCATCTGCTTGGACCATGAGCGGCAACATCAAT 581  
 DB 1 CCTCCAGCGCTTGGCGCTTCTTGACGAGCGCTTACATCACT 42

RESULT 2  
 LOCUS AR085813 45 bp DNA linear PAT 07-SEP-2000  
 DEFINITION Sequence 8 from patent US 5985281.  
 ACCESSION AR085813  
 VERSION AR085813.1 GI:10012579  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.

REFERENCE  
 1 (bases 1 to 45)  
 Taylor, J., Eggle, H., Johannes, T., Tarragona-Fiol, A.,  
 Rablin, B., Robert, Boyle, F., Thomas, J., Frederick, J.,  
 Blakey, D., Charles, Marsham, P., Robert, Heaton, D., William, J.,  
 Davies, P., Huw, Slater, A., Michael, and Hennequin, L., Francois, Andre.

TITLE  
 JOURNAL  
 FEATURES  
 source 1..45  
 /organism="unknown"

BASE COUNT 3 a 11 c 15 g 16 t  
 ORIGIN

Query Match 1.9%; Score 20.6; DB 6; Length 45;  
 Best Local Similarity 85.2%; Pred. No. 5.3e+05;  
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 807 TGGTCGTCGATGCGCATGAGCGCTGG 833  
 DB 19 TGGTCGTCGATGCGCATGAGCGCTGG 45

RESULT 3  
 LOCUS A05545 45 bp DNA linear PAT 05-MAY-1993  
 DEFINITION Oligonucleotide L3 for annealing and isolation of Fused Monoclonal  
 Gene.  
 ACCESSION A05545  
 VERSION A05545.1 GI:345087  
 KEYWORDS  
 SOURCE synthetic construct.  
 ORGANISM synthetic construct.  
 REFERENCE  
 1 (bases 1 to 45)

AUTHORS  
 TITLE  
 JOURNAL  
 FEATURES  
 source 1..45  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630"

PREPARATION OF NOVEL PROTEIN SWEETENERS  
 Patent: WO 8810303-A 10 29-DEC-1988;  
 Location/Qualifiers  
 BASE COUNT 11 a 10 c 5 g 19 t  
 ORIGIN

Query Match 1.9%; Score 20.2; DB 6; Length 45;  
 Best Local Similarity 68.3%; Pred. No. 7e+05;  
 Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 392 AGCAACAATATGCTCACTAGTGTGATGGAACATCAAA 432  
 DB 44 AGCAACAAGATTGCTCACTATATGATGATGACCTTCAACA 4



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	Best local similarity	68.3%	Pred. NO.	7e+05	
Matches	28	Conservative	0	Mismatches	13
				Indels	0
				Gaps	0
OY	392 AGGCACCAATTATGTCCTACTAAGGTGGATGAACCATCAAAA	432			
Db	44 AAAAAACAAGATTGGTCCAATATGGTAGATGCACTTCCACA	4			
RESULT 6					
AXI16244/c					
LOCUS	AXI16244	27 bp	DNA		
DEFINITION	Sequence 1367 from Patent WO0129262.		linear		PAT 11-MAY-2001
ACCESSION	AXI16244				
VERSION	AXI16244.1	GI:14033186			
KEYWORDS	.				
SOURCE	synthetic construct.				
ORGANISM	artificial sequence.				
	artificial sequence.				
REFERENCE	I (bases 1 to 27)				
AUTHORS	Picoult-Newburg,L. and Pohl,M.				

	1.8%;	Score 19.4;	DB 9;	Length 37;
Query Match	Similarity 70.3%;	Pred. No. 1.2e+06;		
Best Local				
Matches 26;	Conservative 0;	Mismatches 11;	Indels 0;	Gaps 0;
QY 139	ACAGAGGTGGTTTGGCATCACTAATCGCCACGAGG	175		
Db 37	AAAGAGCACCATTCTGGCCATCTCCATAAAGCCACGAGG	1		



BASE COUNT		9	a	13	c	16	g	12	t	
ORIGIN		/gene="VH7183-D-J"								
Query Match		1.7%; Score 19; DB 10; Length 50;								
Best Local Similarity		65.1%; Pred. No. 1.7e+06;								
Matches	28;	Conservative	0;						Mismatches 15;	Indels 0;
OY	516	CAATGCTGGATTACTTACTGAACCATCTTCCTTGACC GC 558								
DB	2	CAAGACTGGGATTTCCTTACTGGGCCAAGGACCTCTGTGCAC 44								
RESULT 15										
LOCUS	A90855						29 bp	DNA	linear	PAT 22-JAN-2000
DEFINITION	Sequence 24 from Patent WO9830582.									
ACCESSION	A90855									
VERSION	A90855.1					GI:6739256				
KEYWORDS	.									
SOURCE	unidentified.									
ORGANISM	unidentified									
REFERENCE	1	(bases 1 to 29)								
AUTHORS	Lavallie,E.R. and Merberg,D.									
TITLE	SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM;									
JOURNAL	Patent: WO 9830582-A 24 16-JUL-1998;									
GENETICS	INST (US)									
FEATURES	Location/Qualifiers									
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ORIGIN						7	g		11	t
										1 others
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Best Local Similarity		90.9%; Pred. No. 1.8e+06;								
Matches	20;	Conservative	0;						Mismatches 2;	Indels 0;
Gaps	0;									
OY	977	TCCTGGGAGAGATGTCATGT 998								
DB	7	TCCTGGTAGAGATGTCATGT 28								
RESULT 16										
LOCUS	AX202646						34 bp	DNA	linear	PAT 30-AUG-2001
DEFINITION	Sequence 119 from Patent WO0153480.									
ACCESSION	AX202646									
VERSION	AX202646.1					GI:15392330				
KEYWORDS	.									
SOURCE	synthetic construct.									
ORGANISM	synthetic construct									
REFERENCE	artificial sequence.									
AUTHORS	1	(bases 1 to 34)								
TITLE	Choo,T., King,A. and Moore,M.T.									
JOURNAL	Nucleic acid binding polypeptides characterized by flexible linkers									
CONNECTION	connected nucleic acid binding modules									
PATENT	Patent: WO 0153480-A 119 26-JUL-2001;									
GENDAQ	Gendag Limited (GB)									
FEATURES	location/Qualifiers									
source	1..34					/organism="synthetic construct"				
						/db_xref="taxon:32630"				
						/note="Primer"				
BASE COUNT	4	a				10	g		13	t
ORIGIN						7	c			
Query Match		1.7%; Score 18.8; DB 6; Length 34;								
Best Local Similarity		76.7%; Pred. No. 1.8e+06;								
Matches	23;	Conservative	0;						Mismatches 7;	Indels 0;
Gaps	0;									
OY	634	GTCCCTCAGGTTTTTGATGGATTTGGCT 663								



SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 34)  
AUTHORS Innis,M.A. and Creasey,A.A.  
TITLE Chimeric proteins  
JOURNAL Patent: US 5589359-A 28 31-DEC-1996;  
FEATURES Location/Qualifiers  
source 1..34  
BASE COUNT 8 a 12 c 6 g 8 t  
ORIGIN

Query Match 1.7%; Score 18.6; DB 6; Length 34;  
Best Local Similarity 72.7%; Pred. No. 2.1e+06;  
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 510 CAAGTCAATGCTGGGATTACTACTGACCC 542  
1 CCAGCTCAATGCTGTGAATACTCCCTGACTCC 33

RESULT 22  
LOCUS 184688 34 bp DNA linear PAT 04-APR-1998  
DEFINITION Sequence 28 from patent US 5696088.  
ACCESSION 184688  
VERSION 184688.1 GI:3022208  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 34)  
AUTHORS Innis,M.A. and Creasey,A.A.  
TITLE Chimeric proteins  
JOURNAL Patent: US 5696088-A 28 09-DEC-1997;  
FEATURES Location/Qualifiers  
source 1..34  
BASE COUNT 8 a 12 c 6 g 8 t  
ORIGIN

Query Match 1.7%; Score 18.6; DB 6; Length 34;  
Best Local Similarity 72.7%; Pred. No. 2.1e+06;  
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 510 CAAGTCAATGCTGGGATTACTACTGACCC 542  
1 CCAGCTCAATGCTGTGAATACTCCCTGACTCC 33

RESULT 23  
LOCUS AX273757 38 bp mRNA linear PAT 29-OCT-2001  
DEFINITION Sequence 1326 from Patent WO0162911.  
ACCESSION AX273757  
VERSION AX273757.1 GI:16546494  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (sites)  
AUTHORS Jarvis,T., von Carlowitz,I., Mswiggen,J.A., Hamlin,P.A. and Ellis,J.H.  
TITLE Method and reagent for the inhibition of grid  
JOURNAL Patent: WO 0162911-A 1326 30-AUG-2001.  
FEATURES RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)  
source 1..38  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Enzymatic Nucleic Acid"  
modified\_base 31

BASE COUNT 6 a /mod\_base=i 8 c 13 g 10 t 1 others  
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Matches 24; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 806 TTGGTCTGATGTGCCATTGACCTGGGTGTGT 839  
3 TTGGTCTGATGTGCCATTGACCTGGGTGTGT 36

RESULT 24  
LOCUS AR030770 45 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 9 from patent US 5861309.  
ACCESSION AR030770  
VERSION AR030770.1 GI:5943984  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 45)  
AUTHORS Bard,J.A., Weinschenk,R.L. and Forray,C.  
TITLE DNA encoding human alpha 1 adrenergic receptors  
JOURNAL Patent: US 5861309-A 9 19-JAN-1999;  
FEATURES Location/Qualifiers  
source 1..45  
BASE COUNT 5 a 15 c 18 g 7 t  
ORIGIN

Query Match 1.7%; Score 18.6; DB 6; Length 45;  
Best Local Similarity 65.9%; Pred. No. 2.2e+06;  
Matches 27; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 135 GGTACAGAGGTGTTGGCTATCACTATGCCACAGG 175  
5 GGCTCCGAGGTGTGTGCTGCATCCACTGTCGGCGCG 45

RESULT 25  
LOCUS AR101774 45 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 9 from patent US 6083705.  
ACCESSION AR101774  
VERSION AR101774.1 GI:12812572  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 45)  
AUTHORS Bard,J.A., Weinschenk,R.L. and Forray,C.  
TITLE DNA encoding human alpha 1 adrenergic receptors and uses thereof  
JOURNAL Patent: US 6083705-A 9 04-JUL-2000;  
FEATURES Location/Qualifiers  
source 1..45  
BASE COUNT 5 a 15 c 18 g 7 t  
ORIGIN

Query Match 1.7%; Score 18.6; DB 6; Length 45;  
Best Local Similarity 65.9%; Pred. No. 2.2e+06;  
Matches 27; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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5 GGCTCCGAGGTGTGTGCTGCATCCACTGTCGGCGCG 45

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Job time : 1811 secs

Wed Oct 23 09:10:11 2002

us-09-374-967-1.max.rge

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Page 14

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: October 22, 2002, 13:38:26 : Search time 192 Seconds

(without alignments)  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21.2	2.0	42	19	AAV02044
2	20.6	1.9	45	17	AAAT42481
3	20.6	1.9	50	22	AAAL30023
4	20.2	1.9	41	24	ABA03581
5	20.2	1.9	41	24	ABA03582
6	20.2	1.9	45	17	AAAT1588
7	20.2	1.9	50	19	AAV98928
8	19.8	1.8	50	13	AAAN20147
9	19.6	1.8	27	21	AAAI0655

C 10	19.6	1.8	27	22	AAH38571	SNP specific SNPE
C 11	19.6	1.8	47	21	AAZ68783	Human map-related
C 12	19.4	1.8	47	16	AAAT6132	Substance P bindin
C 13	19.2	1.8	42	21	AAAO7196	PCR primer for P4
C 14	19.2	1.8	42	21	AAZ98251	P. oleovarans phac
C 15	19.2	1.8	48	13	AAQ29922	Fruit fly cuticle
C 16	19.2	1.8	48	13	AAQ81980	Native D. melanoga
C 17	19.2	1.8	50	19	AAV96340	Solanidine glucosy
C 18	19.2	1.8	50	22	AAAL28793	Human SNP oligonuc
C 19	19.2	1.8	35	22	AAAD08176	Human c-fos hairpi
C 20	19.1	1.7	37	21	AAZ49438	PCR primer MU-rele
C 21	19.1	1.7	45	24	ABLI31957	PCR primer FOKI loo
C 22	19.1	1.7	47	19	AAV03973	PCR probe SODEX-3-
C 23	19.1	1.7	47	21	AAZ69509	Human map-related
C 24	18.8	1.7	29	19	AAV40515	Human secreted pro
C 25	18.8	1.7	34	22	AAH23347	Nucleotide sequenc
C 26	18.8	1.7	47	21	AAZ87603	Murine MBP coding
C 27	18.8	1.7	48	20	AAV89539	EST clone CQ333.
C 28	18.8	1.7	50	19	AAV95558	Human c-fos hairpi
C 29	18.8	1.7	50	20	AAZ09316	Ubiquitin fusion p
C 30	18.8	1.7	50	21	AAV7506	Human glycoprotein
C 31	18.8	1.7	50	22	AAZ60342	Synthetic oligonuc
C 32	18.6	1.7	27	21	AAZ47740	Primer used to gen
C 33	18.6	1.7	28	21	AAZ46073	PCR primer used to
C 34	18.6	1.7	28	21	AAZ46075	PCR primer used to
C 35	18.6	1.7	28	22	AAZ82328	Chloroform-COR box
C 36	18.6	1.7	34	24	AAZ25847	Chloroform virus-pd
C 37	18.6	1.7	41	22	AAH77463	Human signal trans
C 38	18.6	1.7	41	22	AAH77463	Human setine/threo
C 39	18.6	1.7	41	22	AAH77463	Primer for alpha 1
C 40	18.6	1.7	45	22	AAO63170	Human alpha-1 adre
C 41	18.6	1.7	45	22	AAO63170	3'-5' sequence of p
C 42	18.6	1.7	47	12	AAQ21541	Human map-related
C 43	18.6	1.7	47	14	AAQ42682	Human EGF-R hairpi
C 44	18.6	1.7	47	21	AAZ67479	Potato citrate syn
C 45	18.6	1.7	50	19	AAV98883	Human SNP oligonuc
C 46	18.6	1.7	50	19	AAV98883	Translocation junc
C 47	18.6	1.7	50	22	AAH29145	Scal restriction e
C 48	18.6	1.7	50	22	AAH29145	Primer D1 to ampli
C 49	18.6	1.7	50	22	AAH29145	Human map-related
C 50	18.4	1.7	36	18	AAAT70168	Human map-related
C 51	18.4	1.7	42	21	AAZ65942	Human map-related
C 52	18.4	1.7	47	21	AAZ68110	Human map-related
C 53	18.4	1.7	50	22	AAH29392	Human SNP oligonuc
C 54	18.4	1.7	50	22	AAH29392	Human SNP oligonuc
C 55	18.2	1.7	33	22	AAI71569	Human humslah prot
C 56	18.2	1.7	40	21	AAAO6820	Primer 3 used to c
C 57	18.2	1.7	42	14	AAO36897	RG677, a mutagenic
C 58	18.2	1.7	47	21	AAZ65117	Synthetic F13 gene
C 59	18.2	1.7	47	21	AAZ65117	Human map-related
C 60	18.2	1.7	50	19	AAV98886	Human EGF-R hairpi
C 61	18.2	1.7	50	19	AAV95581	Human c-fos hairpi
C 62	18.2	1.7	50	19	AAV95581	Human c-fos hairpi
C 63	18.2	1.7	50	22	AAAL28631	Human SNP oligonuc
C 64	18.2	1.7	50	22	AAH89669	Human protease cod
C 65	18.2	1.7	50	23	ABLI00122	Human silent nonco
C 66	18.2	1.7	34	20	AAH08922	PCR primer for fru
C 67	18.2	1.7	38	19	AAV25365	PCR primer used to
C 68	18.2	1.7	41	22	AAH44431	Human chromo domat
C 69	18.2	1.7	45	18	AAO69284	Human aldolase B g
C 70	18.2	1.7	45	18	AAO69284	Human aldolase B g
C 71	18.2	1.7	45	19	AAV34464	Human aldolase B g
C 72	18.2	1.7	45	20	AAV34464	MHC class I chain-
C 73	18.2	1.7	47	21	AAZ66407	Test sequence from
C 74	18.2	1.7	47	21	AAZ66407	Human map-related
C 75	18.2	1.7	50	15	AAZ66469	Human map-related
C 76	18.2	1.7	50	18	AAZ66469	Human aldolase B (
C 77	18.2	1.7	50	18	AAAT64127	Human aldolase B (
C 78	18.2	1.7	50	20	AAAT64127	Test sequence from
C 79	18.2	1.7	50	24	ABLI31939	Target DNA oligonu
C 80	18.2	1.7	50	24	ABLI31939	Target DNA oligonu
C 81	18.2	1.7	50	24	ABLI31983	Antisense oligonuc
C 82	17.8	1.6	30	15	AAO65302	NO-synthase PCR pr

C 83	17.8	1.6	30	17	AAAT60537	Primer #1 for huma	C 156	17.2	1.6	31	20	AAAT21709	Competitor oligo C
C 84	17.8	1.6	39	19	AAAT61754	A. victoria green	C 157	17.2	1.6	34	16	AAAT86214	Sindbis/PV non-cod
C 85	17.8	1.6	40	17	AAAT70703	Fibrin clot bindin	C 158	17.2	1.6	34	16	AAAT86210	Sindbis/PV non-cod
C 86	17.8	1.6	40	21	AAAT296062	Polynucleotide seq	C 159	17.2	1.6	34	17	AAAT31157	Polymavirus prime
C 87	17.8	1.6	41	19	AAAT50599	Brassica sp. polym	C 160	17.2	1.6	34	17	AAAT31160	Polymavirus forma
C 88	17.8	1.6	41	22	AAAT49805	Human trans-glutam	C 161	17.2	1.6	34	19	AAAT63984	Mycoobacterium tube
C 89	17.8	1.6	44	18	AAAT60603	CDNA encoding Mage	C 162	17.2	1.6	34	19	AAAT60191	Forward primer Pyb
C 90	17.8	1.6	45	15	AAAT63793	Bovine Erypsin III	C 163	17.2	1.6	34	19	AAAT60194	Reverse primer use
C 91	17.8	1.6	45	19	AAAT65131	Site of the fusion	C 164	17.2	1.6	34	19	AAAT42432	Forward PCR primer
C 92	17.8	1.6	47	21	AAAT66212	Human map-related	C 165	17.2	1.6	34	19	AAAT42435	PCR primer for clo
C 93	17.8	1.6	47	21	AAAT66343	Human map-related	C 166	17.2	1.6	34	20	AAAT81048	Forward primer Pyb
C 94	17.8	1.6	47	21	AAAT68139	Human map-related	C 167	17.2	1.6	34	20	AAAT70752	Forward PCR primer
C 95	17.8	1.6	47	21	AAAT69467	Human map-related	C 168	17.2	1.6	34	20	AAAT70755	Forward PCR primer
C 96	17.8	1.6	48	23	AAAT69467	Human map-related	C 169	17.2	1.6	34	21	AAAT29849	Polymavirus non-c
C 97	17.8	1.6	50	19	AAAT98885	Human EGF-R hairpi	C 170	17.2	1.6	34	21	AAAT29852	Sindbis PCR primer
C 98	17.8	1.6	50	22	AAAT33838	Human SNP oligonuc	C 171	17.2	1.6	34	21	AAAT29879	Polymavirus non-c
C 99	17.8	1.6	50	22	AAAT33838	Solanidin glucosyl	C 172	17.2	1.6	34	21	AAAT29887	Sindbis PCR primer
C 100	17.6	1.6	27	19	AAAT96087	Campor thioestera	C 173	17.2	1.6	37	18	AAAT63422	Polymavirus non-c
C 101	17.6	1.6	38	17	AAAT32237	Fibrin clot bindin	C 174	17.2	1.6	37	18	AAAT63422	Sindbis PCR primer
C 102	17.6	1.6	40	17	AAAT70665	Ampr fragment PCR	C 175	17.2	1.6	37	20	AAAT63422	Primer #1 for prep
C 103	17.6	1.6	40	19	AAAT58112	Ampr fragment PCR	C 176	17.2	1.6	37	23	AAAT63422	FKBP-12 PCR primer
C 104	17.6	1.6	40	19	AAAT58183	Ampr sense PCR prim	C 177	17.2	1.6	39	21	AAAT63422	PCR primer used to
C 105	17.6	1.6	41	19	AAAT58125	Ampr+COLE1 PCR pri	C 178	17.2	1.6	40	16	AAAT51507	Human CD20 G-Cleav
C 106	17.6	1.6	41	19	AAAT58147	PCR primer designa	C 179	17.2	1.6	40	19	AAAT30880	Portion-3 of 3'UTR
C 107	17.6	1.6	41	19	AAAT58094	PCR primer designa	C 180	17.2	1.6	40	22	AAAT29791	FKBP N-terminal de
C 108	17.6	1.6	42	21	AAAT98259	Z. ramigera phbc g	C 181	17.2	1.6	40	22	AAAT91416	Fragment of CDNA e
C 109	17.6	1.6	43	24	AAAT81235	P53 mutation detec	C 182	17.2	1.6	41	19	AAAT91416	Human p53UBC hybri
C 110	17.6	1.6	43	24	AAAT29368	DNA fragment of JN	C 183	17.2	1.6	41	19	AAAT51507	R. reniformis GFP
C 111	17.6	1.6	44	21	AAAT29370	Antisense oligo to	C 184	17.2	1.6	41	19	AAAT27136	R. reniformis GFP
C 112	17.6	1.6	44	21	AAAT29370	JNK antisense olig	C 185	17.2	1.6	41	19	AAAT27136	Synthetic human co
C 113	17.6	1.6	44	21	AAAT29370	Human ornithine tr	C 186	17.2	1.6	41	22	AAAT41267	Human CYP2B6 allel
C 114	17.6	1.6	46	18	AAAT63967	Test sequence from	C 187	17.2	1.6	41	22	AAAT41267	Human protein kina
C 115	17.6	1.6	46	20	AAAT12255	Human map-related	C 188	17.2	1.6	42	15	AAAT66427	Krtinase protein 13
C 116	17.6	1.6	47	21	AAAT66415	Human map-related	C 189	17.2	1.6	42	15	AAAT66427	Primer to amplify
C 117	17.6	1.6	47	21	AAAT66415	Human map-related	C 190	17.2	1.6	43	14	AAAT83333	PCR primer for Dro
C 118	17.6	1.6	47	21	AAAT66415	Human map-related	C 191	17.2	1.6	43	14	AAAT83333	DNA fragment encod
C 119	17.6	1.6	50	17	AAAT31226	Ova257-264 constru	C 192	17.2	1.6	45	16	AAAT83333	Sulfolobus solifata
C 120	17.6	1.6	50	17	AAAT31226	Synthetic hairpin	C 193	17.2	1.6	45	17	AAAT16672	Hepatitis C virus
C 121	17.6	1.6	50	17	AAAT31206	Synthetic hairpin	C 194	17.2	1.6	46	21	AAAT01110	Oligo #2, to produ
C 122	17.6	1.6	50	17	AAAT31211	Solaniidine glucosy	C 195	17.2	1.6	47	20	AAAT01110	Primer for DNA enc
C 123	17.6	1.6	50	19	AAAT96344	Liposome membrane	C 196	17.2	1.6	47	20	AAAT01110	Probe for human PG
C 124	17.6	1.6	50	21	AAAT47142	Human SNP oligonuc	C 197	17.2	1.6	47	21	AAAT67418	Human map-related
C 125	17.6	1.6	50	22	AAAT34142	Tobacco ringspot v	C 198	17.2	1.6	47	22	AAAT12943	Single stranded DN
C 126	17.6	1.6	50	22	AAAT34142	Tobacco ringspot v	C 199	17.2	1.6	47	22	AAAT34903	Enzymatic DNA 107m
C 127	17.6	1.6	50	22	AAAT31382	Tobacco mosaic vir	C 200	17.2	1.6	48	17	AAAT73974	HIV-1 amplicon pre
C 128	17.6	1.6	50	22	AAAT31387	Tobacco ringspot v	C 201	17.2	1.6	48	20	AAAT73974	VEGF 2'-NH2-RNA nu
C 129	17.6	1.6	50	22	AAAT31388	Tobacco ringspot v	C 202	17.2	1.6	48	21	AAAT92246	Human EGF-R hairpi
C 130	17.6	1.6	50	22	AAAT31396	Tobacco ringspot v	C 203	17.2	1.6	49	22	AAAT92246	Human EGF-R hairpi
C 131	17.6	1.6	50	22	AAAT31396	Tobacco ringspot v	C 204	17.2	1.6	50	19	AAAT98898	Human EGF-R hairpi
C 132	17.6	1.6	50	22	AAAT313216	Tobacco ringspot v	C 205	17.2	1.6	50	19	AAAT98898	Human EGF-R hairpi
C 133	17.6	1.6	50	22	AAAT313216	Tobacco ringspot v	C 206	17.2	1.6	50	19	AAAT98898	Human EGF-R hairpi
C 134	17.6	1.6	50	22	AAAT313216	Tobacco ringspot v	C 207	17.2	1.6	50	20	AAAT98898	Human EGF-R hairpi
C 135	17.6	1.6	50	22	AAAT313216	Tobacco ringspot v	C 208	17.2	1.6	50	20	AAAT98898	Human EGF-R hairpi
C 136	17.6	1.6	50	22	AAAT313216	Tobacco ringspot v	C 209	17.2	1.6	50	20	AAAT98898	Human EGF-R hairpi
C 137	17.6	1.6	50	22	AAAT313216	Tobacco ringspot v	C 210	17.2	1.6	50	20	AAAT98898	Human EGF-R hairpi
C 138	17.6	1.6	50	22	AAAT313216	Tobacco ringspot v	C 211	17.2	1.6	50	20	AAAT98898	Human EGF-R hairpi
C 139	17.6	1.6	50	22	AAAT313216	Tobacco ringspot v	C 212	17.2	1.6	50	20	AAAT98898	Human EGF-R hairpi
C 140	17.6	1.6	50	22	AAAT313216	Tobacco ringspot v	C 213	17.2	1.6	50	20	AAAT98898	Human EGF-R hairpi
C 141	17.6	1.6	50	22	AAAT313216	Tobacco ringspot v	C 214	17.2	1.6	50	20	AAAT98898	Human EGF-R hairpi
C 142	17.6	1.6	50	22	AAAT313216	Tobacco ringspot v	C 215	17.2	1.6	50	20	AAAT98898	Human EGF-R hairpi
C 143	17.6	1.6	50	22	AAAT313216	Tobacco ringspot v	C 216	17.2	1.6	50	20	AAAT98898	Human EGF-R hairpi
C 144	17.6	1.6	50	22	AAAT313216	Tobacco ringspot v	C 217	17.2	1.6	50	20	AAAT98898	Human EGF-R hairpi
C 145	17.6	1.6	50	22	AAAT313216	Tobacco ringspot v	C 218	17.2	1.6	50	20	AAAT98898	Human EGF-R hairpi
C 146	17.6	1.6	50	22	AAAT313216	Tobacco ringspot v	C 219	17.2	1.6	50	20	AAAT98898	Human EGF-R hairpi
C 147	17.6	1.6	50	22	AAAT313216	Tobacco ringspot v	C 220	17.2	1.6	50	20	AAAT98898	Human EGF-R hairpi
C 148	17.6	1.6	50	22	AAAT313216	Tobacco ringspot v	C 221	17.2	1.6	50	20	AAAT98898	Human EGF-R hairpi
C 149	17.6	1.6	50	22	AAAT313216	Tobacco ringspot v	C 222	17.2	1.6	50	20	AAAT98898	Human EGF-R hairpi
C 150	17.6	1.6	50	22	AAAT313216	Tobacco ringspot v	C 223	17.2	1.6	50	20	AAAT98898	Human EGF-R hairpi
C 151	17.6	1.6	50	22	AAAT313216	Tobacco ringspot v	C 224	17.2	1.6	50	20	AAAT98898	Human EGF-R hairpi
C 152	17.6	1.6	50	22	AAAT313216	Tobacco ringspot v	C 225	17.2	1.6	50	20	AAAT98898	Human EGF-R hairpi
C 153	17.6	1.6	50	22	AAAT313216	Tobacco ringspot v	C 226	17.2	1.6	50	20	AAAT98898	Human EGF-R hairpi
C 154	17.6	1.6	50	22	AAAT313216	Tobacco ringspot v	C 227	17.2	1.6	50	20	AAAT98898	Human EGF-R hairpi
C 155	17.6	1.6	50	22	AAAT313216	Tobacco ringspot v	C 228	17.2	1.6	50	20	AAAT98898	Human EGF-R hairpi





375	16.6	1.5	46	19	AAAT96170	5' intron sequence
376	16.6	1.5	46	21	AAZ45368	PCR primer BXM5.10
377	16.6	1.5	46	22	AAH41620	Hco7, Hco12 and Hc
378	16.6	1.5	46	22	AAH29966	Hco7, Hco12 and Hc
379	16.6	1.5	47	13	AAO28030	Primer CASOL3742.
380	16.6	1.5	47	15	AAO69418	Human H2b histone
381	16.6	1.5	47	18	AAAT63880	Human H2b histone
382	16.6	1.5	47	20	AAZ01111	Probe for human PG
383	16.6	1.5	47	20	AAZ52607	Human genome biall
384	16.6	1.5	47	20	AAZ52557	Human genome biall
385	16.6	1.5	47	20	AAZ52557	Test sequence from
386	16.6	1.5	47	20	AAZ52557	Human map-related
387	16.6	1.5	47	21	AAZ67048	Human map-related
388	16.6	1.5	47	21	AAZ67533	Sequence of the ju
389	16.6	1.5	48	13	AAO22992	Fruit fly cuticle
390	16.6	1.5	48	16	AAO94182	Transmembrane olig
391	16.6	1.5	48	21	AAO87775	SNORF36 receptor i
392	16.6	1.5	49	17	AAAT31212	Synthetic hairpin
393	16.6	1.5	49	22	AAO09773	Primer #2 used in
394	16.6	1.5	50	15	AAO74372	Capture probe Bb50
395	16.6	1.5	50	19	AAV98948	Human EGF-R hairpi
396	16.6	1.5	50	19	AAV98916	Human EGF-R hairpi
397	16.6	1.5	50	19	AAV95567	Human c-fos hairpi
398	16.6	1.5	50	19	AAV97177	Potato citrate syn
399	16.6	1.5	50	19	AAV97178	Microsatellite rep
400	16.6	1.5	50	21	AAZ18640	Human ASH1 polymo
401	16.6	1.5	50	21	AAZ80547	Human MLH1 gene ex
402	16.6	1.5	50	22	AAZ68887	Human SNP oligonuc
403	16.6	1.5	50	22	AAZ80588	Human SNP oligonuc
404	16.6	1.5	50	22	AAZ8581	Human SNP oligonuc
405	16.6	1.5	50	22	AAZ34084	Tobacco ringspot v
406	16.6	1.5	50	22	AAZ13237	Human silent SNP c
407	16.6	1.5	50	22	AAZ14733	1467-03 PCR primer
408	16.6	1.5	50	22	AAAD03091	SNP specific lower
409	16.6	1.5	50	22	AAAD0466	Lettuce Infectious
410	16.6	1.5	50	22	AAO83173	Mouse flk-1 VEGF r
411	16.6	1.5	50	22	AAZ72138	Wheat oxalate oxid
412	16.6	1.5	50	22	AAZ17799	Wheat oxalate oxid
413	16.6	1.5	50	22	AAZ02835	Integrin subunit b
414	16.6	1.5	50	22	AAZ2420	Oestrogen receptor
415	16.6	1.5	50	22	AAZ24464	5' primer used to
416	16.6	1.5	50	22	AAAD0328	Human diallelic po
417	16.6	1.5	50	22	AAO8424	Human diallelic po
418	16.6	1.5	50	22	AAO8424	Human diallelic po
419	16.6	1.5	50	22	AAO8424	Human diallelic po
420	16.6	1.5	50	22	AAO8424	Human diallelic po
421	16.6	1.5	50	22	AAO8424	Human diallelic po
422	16.6	1.5	50	22	AAO8424	Human diallelic po
423	16.6	1.5	50	22	AAO8424	Human diallelic po
424	16.6	1.5	50	22	AAO8424	Human diallelic po
425	16.6	1.5	50	22	AAO8424	Human diallelic po
426	16.6	1.5	50	22	AAO8424	Human diallelic po
427	16.6	1.5	50	22	AAO8424	Human diallelic po
428	16.6	1.5	50	22	AAO8424	Human diallelic po
429	16.6	1.5	50	22	AAO8424	Human diallelic po
430	16.6	1.5	50	22	AAO8424	Human diallelic po
431	16.6	1.5	50	22	AAO8424	Human diallelic po
432	16.6	1.5	50	22	AAO8424	Human diallelic po
433	16.6	1.5	50	22	AAO8424	Human diallelic po
434	16.6	1.5	50	22	AAO8424	Human diallelic po
435	16.6	1.5	50	22	AAO8424	Human diallelic po
436	16.6	1.5	50	22	AAO8424	Human diallelic po
437	16.6	1.5	50	22	AAO8424	Human diallelic po
438	16.6	1.5	50	22	AAO8424	Human diallelic po
439	16.6	1.5	50	22	AAO8424	Human diallelic po
440	16.6	1.5	50	22	AAO8424	Human diallelic po
441	16.6	1.5	50	22	AAO8424	Human diallelic po
442	16.6	1.5	50	22	AAO8424	Human diallelic po
443	16.6	1.5	50	22	AAO8424	Human diallelic po
444	16.6	1.5	50	22	AAO8424	Human diallelic po
445	16.6	1.5	50	22	AAO8424	Human diallelic po
446	16.6	1.5	50	22	AAO8424	Human diallelic po
447	16.6	1.5	50	22	AAO8424	Human diallelic po

C 521	16.2	1.5	41	17	AAT27080	S. hyicus lipase ge
C 522	16.2	1.5	41	18	AAT94018	Primer for TPO/ACG
C 523	16.2	1.5	41	19	AAV51243	Maize polymorphic
C 524	16.2	1.5	41	19	AAV51244	Brassica sp. polym
C 525	16.2	1.5	41	19	AAV50618	Sense primer for E
C 526	16.2	1.5	41	21	AAV51257	Bacterial trans-glytam
C 527	16.2	1.5	41	22	AAH49804	Human serine/threo
C 528	16.2	1.5	41	22	AAH50086	Arabidopsis thalia
C 529	16.2	1.5	41	22	ABA82735	PCR primer for thalia
C 530	16.2	1.5	42	24	AAH64873	Dopamine receptor
C 531	16.2	1.5	43	21	AAZ5180	Kappa light chain
C 532	16.2	1.5	43	21	AAZ5183	Endoglycoceramidas
C 533	16.2	1.5	44	18	AAO35146	Primer O-553 used
C 534	16.2	1.5	44	18	AAT58824	Oligonucleotide us
C 535	16.2	1.5	44	18	AAT6052	DNA encoding signa
C 536	16.2	1.5	44	18	AAV39256	Leader sequence fo
C 537	16.2	1.5	44	18	AAV39256	RNase-T1 coding re
C 538	16.2	1.5	44	18	AAV39256	RNase-T1 mutant co
C 539	16.2	1.5	44	18	AAV39256	RNase-T1 mutant co
C 540	16.2	1.5	44	18	AAV39256	Oligonucleotide 91
C 541	16.2	1.5	44	18	AAV39256	Primer #3. Amycol
C 542	16.2	1.5	44	18	AAV39256	Probe for human P6
C 543	16.2	1.5	44	18	AAV39256	Human map-related
C 544	16.2	1.5	44	18	AAV39256	Human map-related
C 545	16.2	1.5	44	18	AAV39256	Human map-related
C 546	16.2	1.5	44	18	AAV39256	Human map-related
C 547	16.2	1.5	44	18	AAV39256	Human map-related
C 548	16.2	1.5	44	18	AAV39256	Human map-related
C 549	16.2	1.5	44	18	AAV39256	Human map-related
C 550	16.2	1.5	44	18	AAV39256	Human map-related
C 551	16.2	1.5	44	18	AAV39256	Human map-related
C 552	16.2	1.5	44	18	AAV39256	Human map-related
C 553	16.2	1.5	44	18	AAV39256	Human map-related
C 554	16.2	1.5	44	18	AAV39256	Human map-related
C 555	16.2	1.5	44	18	AAV39256	Human map-related
C 556	16.2	1.5	44	18	AAV39256	Human map-related
C 557	16.2	1.5	44	18	AAV39256	Human map-related
C 558	16.2	1.5	44	18	AAV39256	Human map-related
C 559	16.2	1.5	44	18	AAV39256	Human map-related
C 560	16.2	1.5	44	18	AAV39256	Human map-related
C 561	16.2	1.5	44	18	AAV39256	Human map-related
C 562	16.2	1.5	44	18	AAV39256	Human map-related
C 563	16.2	1.5	44	18	AAV39256	Human map-related
C 564	16.2	1.5	44	18	AAV39256	Human map-related
C 565	16.2	1.5	44	18	AAV39256	Human map-related
C 566	16.2	1.5	44	18	AAV39256	Human map-related
C 567	16.2	1.5	44	18	AAV39256	Human map-related
C 568	16.2	1.5	44	18	AAV39256	Human map-related
C 569	16.2	1.5	44	18	AAV39256	Human map-related
C 570	16.2	1.5	44	18	AAV39256	Human map-related
C 571	16.2	1.5	44	18	AAV39256	Human map-related
C 572	16.2	1.5	44	18	AAV39256	Human map-related
C 573	16.2	1.5	44	18	AAV39256	Human map-related
C 574	16.2	1.5	44	18	AAV39256	Human map-related
C 575	16.2	1.5	44	18	AAV39256	Human map-related
C 576	16.2	1.5	44	18	AAV39256	Human map-related
C 577	16.2	1.5	44	18	AAV39256	Human map-related
C 578	16.2	1.5	44	18	AAV39256	Human map-related
C 579	16.2	1.5	44	18	AAV39256	Human map-related
C 580	16.2	1.5	44	18	AAV39256	Human map-related
C 581	16.2	1.5	44	18	AAV39256	Human map-related
C 582	16.2	1.5	44	18	AAV39256	Human map-related
C 583	16.2	1.5	44	18	AAV39256	Human map-related
C 584	16.2	1.5	44	18	AAV39256	Human map-related
C 585	16.2	1.5	44	18	AAV39256	Human map-related
C 586	16.2	1.5	44	18	AAV39256	Human map-related
C 587	16.2	1.5	44	18	AAV39256	Human map-related
C 588	16.2	1.5	44	18	AAV39256	Human map-related
C 589	16.2	1.5	44	18	AAV39256	Human map-related
C 590	16.2	1.5	44	18	AAV39256	Human map-related
C 591	16.2	1.5	44	18	AAV39256	Human map-related
C 592	16.2	1.5	44	18	AAV39256	Human map-related
C 593	16.2	1.5	44	18	AAV39256	Human map-related



C 813	15.8	1.5	38	19	AAV10833	Human MS2 gene PC	C 886	15.8	1.5	48	22	AA506244	PCR primer attL1TC
C 814	15.8	1.5	38	20	AA60878	NaMG DNA cloning P	C 887	15.8	1.5	48	22	AA506250	PCR primer attL1TC
C 815	15.8	1.5	38	22	AA96177	Human CHX1 ribozym	C 888	15.8	1.5	48	22	AA506255	PCR primer attL1TC
C 816	15.8	1.5	38	22	AA96493	Human CHX1 ribozym	C 889	15.8	1.5	48	22	AA506260	PCR primer attL1TC
C 817	15.8	1.5	38	22	AAH22092	gpi100 CTL epitope	C 890	15.8	1.5	48	22	AA506263	PCR primer attL1TC
C 818	15.8	1.5	38	23	ABK03990	Human NCOG Hammerh	C 891	15.8	1.5	48	22	AA507787	Oligonucleotide #2
C 819	15.8	1.5	38	23	ABK04298	Human NCOG Hammerh	C 892	15.8	1.5	48	22	AA507944	Analys capture pr
C 820	15.8	1.5	38	23	ABK04426	Human NCOG Hammerh	C 893	15.8	1.5	48	12	AAQ12944	HIV analyte captu
C 821	15.8	1.5	38	23	ABK04863	Human NCOG Hammerh	C 894	15.8	1.5	49	18	AAAT74394	Human CD4 N-termi
C 822	15.8	1.5	38	23	ABK05034	Human NCOG Inozyme	C 895	15.8	1.5	49	20	AA555753	PCR mutagenic olig
C 823	15.8	1.5	38	23	ABK07921	Human NCOG Inozyme	C 896	15.8	1.5	49	20	AA557304	Oligonucleotide CD
C 824	15.8	1.5	39	20	AAZ26942	Human CD20 Hammerh	C 897	15.8	1.5	49	24	AA563635	Arabidopsis antis
C 825	15.8	1.5	39	22	AAZ26942	Human chromosome 1	C 898	15.8	1.5	50	13	AAQ12685	Rei light chain va
C 826	15.8	1.5	40	11	AAO05723	Human chromosome-1	C 899	15.8	1.5	50	15	AAO54486	Excitatory amino a
C 827	15.8	1.5	40	13	AAO05723	Human chromosome-1	C 900	15.8	1.5	50	15	AAO54487	Excitatory amino a
C 828	15.8	1.5	40	20	AAZ26981	PCR primer 5 to am	C 901	15.8	1.5	50	15	AAO70984	NMO gene specific
C 829	15.8	1.5	40	21	AAZ96046	Human chromosome 1	C 902	15.8	1.5	50	17	AAAT13172	Rat interleukin-1
C 830	15.8	1.5	40	21	AAZ96046	Human chromosome 1	C 903	15.8	1.5	50	18	AAV16123	Staphylococcus aur
C 831	15.8	1.5	40	22	AAAD10609	Polynucleotide seq	C 904	15.8	1.5	50	22	AA127914	Human SNP oligonuc
C 832	15.8	1.5	40	22	AAAF32326	Polynucleotide seq	C 905	15.8	1.5	50	22	AA130946	Human SNP oligonuc
C 833	15.8	1.5	41	14	AAO57536	DNA ligand #15 for	C 906	15.8	1.5	50	22	AA131192	Human SNP oligonuc
C 834	15.8	1.5	41	17	AAAT36099	E. coli AS-dihydro	C 907	15.8	1.5	50	22	AA130946	Human SNP oligonuc
C 835	15.8	1.5	41	17	AAAT12835	PCR primer CLC 27	C 908	15.8	1.5	50	22	AA131192	Human SNP oligonuc
C 836	15.8	1.5	41	19	AAV50592	Primer ISHV-S. S	C 909	15.8	1.5	50	22	AA131809	Human SNP oligonuc
C 837	15.8	1.5	41	19	AAV50592	Brassica sp. polym	C 910	15.8	1.5	50	22	AA132023	Human SNP oligonuc
C 838	15.8	1.5	41	19	AAV47954	Brassica sp. polym	C 911	15.8	1.5	50	22	AA132330	Human SNP oligonuc
C 839	15.8	1.5	41	19	AAV47955	Maize polymorphic	C 912	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 840	15.8	1.5	41	20	AAZ21319	Maize polymorphic	C 913	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 841	15.8	1.5	41	22	ABA92350	Lactococcus lactis	C 914	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 842	15.8	1.5	42	12	AAQ14023	Human glucoprotein	C 915	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 843	15.8	1.5	42	19	AAV33031	X-D-BrdC oligonuc	C 916	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 844	15.8	1.5	42	20	AAV33031	Dirofilaria immitis	C 917	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 845	15.8	1.5	42	21	AAZ96579	HBV detecting prim	C 918	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 846	15.8	1.5	42	22	AAAD13145	T cell antigen rec	C 919	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 847	15.8	1.5	42	24	AAI67839	D. immitis transgl	C 920	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 848	15.8	1.5	43	17	AAAT27748	Neural thread prot	C 921	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 849	15.8	1.5	43	18	AAV09726	Adenovirus minigen	C 922	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 850	15.8	1.5	43	21	AAAD8809	Primer 3883556 F-T	C 923	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 851	15.8	1.5	43	24	AAAD24572	Oligonucleotide #9	C 924	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 852	15.8	1.5	44	14	AAO78507	Human GRP78 NOL1-1	C 925	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 853	15.8	1.5	44	24	AB131948	Bsg1/PvuII loop co	C 926	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 854	15.8	1.5	45	8	AAAT70499	Consensus repeat s	C 927	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 855	15.8	1.5	45	11	AAO05722	Probe 1152 for bas	C 928	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 856	15.8	1.5	45	11	AAO05722	Sequence of an ol	C 929	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 857	15.8	1.5	45	15	AAO63792	Bovine trypsin oli	C 930	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 858	15.8	1.5	45	17	AAAT34175	Encoded reaction c	C 931	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 859	15.8	1.5	45	21	AAAT34175	H. pullorum 16S rR	C 932	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 860	15.8	1.5	46	17	AAAT34745	PCR primer OPR131	C 933	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 861	15.8	1.5	46	22	AAAD15889	Muskemton AOS part	C 934	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 862	15.8	1.5	46	22	AAAD13156	Human membrane-ty	C 935	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 863	15.8	1.5	47	13	AAO35810	HIV-1 env (non-cl	C 936	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 864	15.8	1.5	47	14	AAO35390	PCR primer HIV3BT	C 937	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 865	15.8	1.5	47	15	AAO65399	Human granulocyte	C 938	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 866	15.8	1.5	47	18	AAAT63861	Human GM-CSF gene	C 939	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 867	15.8	1.5	47	21	AAAT7149	Test sequence from	C 940	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 868	15.8	1.5	47	21	AAZ65944	Human map-related	C 941	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 869	15.8	1.5	47	21	AAZ65992	Human map-related	C 942	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 870	15.8	1.5	47	21	AAZ65992	Human map-related	C 943	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 871	15.8	1.5	47	21	AAZ66870	Human map-related	C 944	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 872	15.8	1.5	47	21	AAZ67079	Human map-related	C 945	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 873	15.8	1.5	47	21	AAZ68430	Human map-related	C 946	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 874	15.8	1.5	47	21	AAZ69169	Human map-related	C 947	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 875	15.8	1.5	47	21	AAZ72695	PCR primer used to	C 948	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 876	15.8	1.5	47	21	AAAO8355	Human TGC-440 sect	C 949	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 877	15.8	1.5	47	22	AAAF2031	Adaptor-indexer 11	C 950	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 878	15.8	1.5	48	19	AAV04950	Part of the nucle	C 951	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 879	15.8	1.5	48	20	AAV82069	Chlamydia cryptic	C 952	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 880	15.8	1.5	48	21	AAO55568	Detector oligonuc	C 953	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 881	15.8	1.5	48	21	AAO55568	Mutational attL si	C 954	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 882	15.8	1.5	48	21	AAO55579	Mutational attL si	C 955	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 883	15.8	1.5	48	21	AAO55584	Mutational attL si	C 956	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 884	15.8	1.5	48	21	AAO55587	Mutational attL si	C 957	15.8	1.5	50	22	AA134414	Human SNP oligonuc
C 885	15.8	1.5	48	22	ABAO1068	Korean beef cattle	C 958	15.8	1.5	50	22	AA134414	Human SNP oligonuc

C 959 15.6 1.4 33 16 AA089941  
 C 960 15.6 1.4 33 20 AAX05627  
 C 961 15.6 1.4 33 22 AAH45262  
 C 962 15.6 1.4 34 16 AAT01579  
 C 963 15.6 1.4 34 18 AAT91368  
 C 964 15.6 1.4 34 21 AAC81311  
 C 965 15.6 1.4 34 22 AAT77261  
 C 966 15.6 1.4 34 24 ABA04046  
 C 967 15.6 1.4 35 18 AAT43871  
 C 968 15.6 1.4 35 22 AAH41116  
 C 969 15.6 1.4 35 13 AAO25115  
 C 970 15.6 1.4 36 17 AAT50482  
 C 971 15.6 1.4 36 18 AATV1338  
 C 972 15.6 1.4 36 18 AAT60998  
 C 973 15.6 1.4 36 19 AAV19386  
 C 974 15.6 1.4 36 19 AAV13432  
 C 975 15.6 1.4 36 19 AAV15505  
 C 976 15.6 1.4 36 20 AAX00017  
 C 977 15.6 1.4 36 21 AAX35646  
 C 978 15.6 1.4 37 22 AAH96723  
 C 979 15.6 1.4 38 15 AAO74732  
 C 980 15.6 1.4 38 17 AAX64134  
 C 981 15.6 1.4 38 19 AAV31049  
 C 982 15.6 1.4 38 19 AAV04794  
 C 983 15.6 1.4 39 17 AAT31317  
 C 984 15.6 1.4 39 17 AAT29622  
 C 985 15.6 1.4 39 18 AAT70302  
 C 986 15.6 1.4 39 19 AAV31050  
 C 987 15.6 1.4 39 19 AAV04795  
 C 988 15.6 1.4 39 21 AAZ54806  
 C 989 15.6 1.4 39 22 AAH43931  
 C 990 15.6 1.4 39 22 AAH25167  
 C 991 15.6 1.4 39 22 AAC84462  
 C 992 15.6 1.4 40 21 AAC84833  
 C 993 15.6 1.4 40 21 AAH67001  
 C 994 15.6 1.4 40 21 AAH53326  
 C 995 15.6 1.4 40 21 AAZ47162  
 C 996 15.6 1.4 40 21 AAT73314  
 C 997 15.6 1.4 40 22 AAT73315  
 C 998 15.6 1.4 40 22 AAH21662  
 C 999 15.6 1.4 40 22 AAH21662  
 C 1000 15.6 1.4 40 22 AAD23039

## ALIGNMENTS

Listeria 16S rDNA  
 E. coli aspc gene  
 S-adenosylmethionl  
 Probe for Erb-B2 p  
 Of virus strain N  
 Mouse apoptosis-re  
 Alpha-mannosidase  
 Human CPTP SNP amp  
 Human xenithine deh  
 Murine immunoglobul  
 PCR primer 21/M6  
 Rabbit CPTP HH rib  
 Primer 16418 for g  
 L-galactono-1,4-la  
 Humicola insolens  
 Primer MKA-05 for  
 Primer for adeno-a  
 Aspergillus oryzae  
 Permethrin linker e  
 Human Chk1 ribozym  
 KRCV envelope prim  
 Expression vector  
 Expression vector  
 Primer 95-1458 for  
 Ad5-hexon sequence  
 Glucocorticoid rec  
 Adenovirus Ad5 hex  
 Proopiomelanocortil  
 Expression vector  
 Primer 95-1464 for  
 Neisseria species  
 Cauliflower mosaic  
 PCR primer used to  
 TRK3-death domain  
 Thiamine responsiv  
 CAH target 5; muta  
 Human congenital a  
 Liposome membrane-  
 Human silent SNP c  
 Human silent SNP c  
 Immunoglobulin tra  
 CAH exon 8 mutant

RESULT 1  
 AAV02044  
 AAV02044 standard; DNA: 42 BP.

05-JUN-1998 (first entry)

Epitope-tagged PrP expression cassette constructing mutagenic primer.

Prion: epitope; FLAG; Strept; poly-histidine; haemagglutinin;  
 recombinant; transgenic animal; scrapie; Creutzfeldt-Jakob disease;  
 CJD; bovine spongiform encephalopathy; BSE; PCR primer; ss.

Synthetic.

W09746572-A1.

11-DEC-1997.

29-MAY-1997; 97WO-US09289.

06-JUN-1996; 96US-0660626.

(REGC ) UNIV CALIFORNIA.

XX

PI Cohen FE, Prusiner SB, Scott MR, Telling GC;  
 XX WPT: 1998-042112/04.  
 DR Nucleic acid construct encoding biologically active protein and  
 XX epitope - especially epitope-tagged prion protein  
 PT Example 1: Page 35; 62pp; English.  
 XX  
 PS This mutagenic primer is used in the construction of a FLAG-tagged prion  
 CC protein (PrP) construct by PCR-mediated mutagenesis of a signal peptidase  
 CC sequence. This recombinant nucleic acid construct encoding an epitope-  
 CC tagged prion protein comprises a first nucleic acid sequence encoding  
 CC an amino acid sequence of a biologically active protein fragment and a  
 CC second nucleic acid sequence encoding a heterologous epitope domain. The  
 CC heterologous epitope domain is a peptide selected from a peptide group of  
 CC FLAG, Strept, poly-histidine, human c-myc peptide recognised by monoclonal  
 CC antibody 12CA5. The protein is a natural, synthetic or chimeric PrP  
 CC molecule. The protein has two different three-dimensional conformations  
 CC and the epitope domain is spatially positioned relative to the protein  
 CC such that the epitope domain is more exposed in a first conformation  
 CC relative to a second conformation. The nucleic acid construct may be used  
 CC for the production of transgenic animals or cells that are useful in a  
 CC method for distinguishing between different conformational shapes of a  
 CC protein. These methods are particularly useful in studying diseases  
 CC caused by prion proteins, e.g. Creutzfeldt-Jakob disease (CJD), scrapie  
 CC and bovine spongiform encephalopathy (BSE).  
 CC  
 XX Sequence 42 BP; 6 A; 15 C; 10 G; 11 T; 0 other;  
 SQ  
 Query Match 2.0%; Score 21.2; DB 19; Length 42;  
 Best Local Similarity 69.0%; Pred. No. 7.9e+03;  
 Matches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
 QY 540 CCCATCTGCTTGCACCCGATGAGCTGAGCCCAACATCAT 581  
 DB 1 CCCCTCAGCGTTTGCCGCTTTCAGAGAGGCTTACATCAGT 42  
 RESULT 2  
 AAT42481  
 ID AAT42481 standard; DNA: 45 BP.  
 XX  
 AC AAT42481;  
 XX  
 DT 10-FEB-1997 (first entry)  
 XX  
 DE Primer for chimeric HP-RNase gene construction.  
 XX  
 XX ribonuclease; human; bovine; pancreatic; anti-tumour therapy; ADEPT;  
 KW mustard-ribonucleotide; antibody directed enzyme prodrug therapy;  
 KW anti-neoplastic; prodrug; reverse polarity; ion pair interaction;  
 KW reduced immunogenicity; non-selective triggering; primer;  
 KW polymerase chain reaction; PCR; HP-RNase; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN W09620011-A1.  
 XX  
 PD 04-JUL-1996.  
 XX  
 XX 21-DEC-1995; 95WO-GB02991.  
 PF  
 XX 16-AUG-1995; 95GB-0016810.  
 PR 23-DEC-1994; 94GB-0026192.  
 XX  
 PA (ZENEC) ZENECA LTD.  
 XX  
 XX Blakey DC, Boyle FT, Davies DH, Eggelte HJ, Heaton DW, Am;  
 PI Hennam JF, Hennequin LFA, Marsham PR, Rabin BR, Slater AM;  
 PI Taragona-Fiol A, Taylorson CJ;  
 XX

DR WPI; 1996-321650/32.  
 XX  
 PT Two component system for anti-tumour therapy - comprising targeting  
 PT moiety linked to mutated enzyme which can transform an  
 PT anti-neoplastic product  
 XX  
 PS Reference Example 2; Page 113; 182pp; English.  
 XX  
 CC A two-component system for anti-tumour therapy comprises a targeting  
 CC moiety linked to a mutated enzyme which can transform an anti-neoplastic  
 CC product. The system is based on antibody directed enzyme producting therapy  
 CC (ADPPT) using a non-naturally occurring mutant form of a host enzyme,  
 CC pref. human pancreatic ribonuclease (HP-RNase). The natural host enzyme  
 CC recognises its natural substrate by an ion pair interaction which is  
 CC reversed in the design of the mutated enzyme and complementary producting,  
 CC i.e. the mutation is a polarity change, esp. in its active site, in  
 CC patric. the HP-RNase lysine at position 66 (positive charge) is  
 CC engineered to have a negatively charged amino acid, pref. glutamine. The  
 CC producting is pref. a mustard-ribonucleotide. The reversed polarity  
 CC approach allows choice of charge properties of products (which may or may  
 CC not also possess active transport properties) to block cell entry of the  
 CC product. This gives a wider range of producting/drug options. The HP-RNase  
 CC was genetically engineered for expression in the periplasmic space of  
 CC E. coli, using the bovine pancreatic RNase signal sequence. To overcome  
 CC the lack of expression caused by the presence of positively charged  
 CC amino acids early in the mature HP-RNase the amino acids at positions 4  
 CC and 6 (Arg4 and Lys6 - which act as stop transfer signals preventing  
 CC translocation) were replaced with alanine. The mutated enzyme has  
 CC markedly reduced immunogenicity compared to non-host enzymes. Also  
 CC because the mutated enzyme is non-naturally occurring, non-selective  
 CC triggering of producting activation by natural flora or host enzymes is  
 CC reduced. AAT2460-83 are a set of overlapping primers used to construct  
 CC the chimeric gene encoding the bovine P-RNase signal fused to HP-RNase.  
 XX  
 SQ Sequence 45 BP; 3 A; 11 C; 15 G; 16 T; 0 other;  
 Query Match 1.9%; Score 20.6; DB 17; Length 45;  
 Best Local Similarity 85.2%; Pred. No. 1.3e+04;  
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 807 TGGTCCTGATGTGCGCATTTGGACCTGG 833  
 ||||||| ||||| ||||| ||||| |||||  
 Db 19 TGGTCCTGATGTGCGCATTTGGACCTGG 45  
 RESULT 3  
 AAL30023/C  
 ID AAL30023 standard; DNA; 50 BP.  
 AC AAL30023;  
 DT 24-JAN-2002 (first entry)  
 DE Human SNP oligonucleotide #3231.  
 XX  
 XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;  
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinase; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200147944-A2.  
 PD 05-JUL-2001.  
 XX  
 PF 28-DEC-2000; 2000MO-US35498.  
 XX  
 PR 28-DEC-1999; 99US-0173419.

PR 27-DEC-2000; 2000US-0173419.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Shimkels RA, Leach M;  
 XX  
 DR WPI; 2001-465210/50.  
 XX  
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g.  
 PT cancer, autoimmune diseases and infections -  
 XX  
 PS Claim 1; Page 2313; 4143pp; English.  
 XX  
 CC The present invention relates to oligonucleotides encoding polymorphic  
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
 CC histones, kinases, colony stimulating factors, complement related  
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,  
 CC G-protein coupled receptors and thioesterases. The present sequence is  
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded  
 CC by them may be used in the prevention, diagnosis and treatment of  
 CC diseases associated with inappropriate expression of the proteins listed  
 CC above. Disorders that may be prevented, diagnosed and/or treated include  
 CC multifactorial diseases with a genetic component, such as autoimmune  
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
 CC leukemia), diseases of the nervous system and an infection of pathogenic  
 CC organisms.  
 XX  
 SQ Sequence 50 BP; 9 A; 18 C; 15 G; 8 T; 0 other;  
 Query Match 1.9%; Score 20.6; DB 22; Length 50;  
 Best Local Similarity 74.3%; Pred. No. 1.4e+04;  
 Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 QY 660 TGGTCAGCCTAGGAGTACTTACTGCTGCTGCTC 694  
 ||||||| ||||| ||||| ||||| ||||| |||||  
 Db 43 TGGTCAGCAGGAGGAGTACTTCTGCTGCTGCTC 9  
 RESULT 4  
 ABA03581/C  
 ID ABA03581 standard; DNA; 41 BP.  
 AC ABA03581;  
 DT 04-MAR-2002 (first entry)  
 DE Human Pax protein 12-5 coding sequence probe #1.  
 XX  
 XX Human; Pax protein 12.5; cancer; haemopathy; HIV infection; cytostatic;  
 KW viroicide; immunomodulator; antiinflammatory; haemostatic; anti-HIV;  
 KW inflammation; immune disease; gene therapy; probe; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200181386-A1.  
 PD 01-NOV-2001.  
 XX  
 PF 23-APR-2001; 2001MO-CN00607.  
 XX  
 PR 27-APR-2000; 2000CN-0115455.  
 XX  
 PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.  
 XX  
 PI Mao Y, Xie Y;  
 XX  
 DR WPI; 2002-026143/03.  
 XX  
 PR New human pax protein 12.5 for diagnosing and treating malignant tumor,





PD	16-APR-1982.
XX	
PF	30-DEC-1981; 81BE-0891659.
XX	
PR	31-DEC-1980; 80FI-0004081.
XX	
PR	12-MAR-1982; 82FI-0000860.
XX	
PA	(PALV/) PALVA I.
XX	
PA	(GENE-) GENESIT OY.
XX	
DR	WPI; 1982-37323E/19.
XX	
PT	Protein produ. using bacillus strain bacteria - by splitting the
PT	alpha-amylase bacillus gene, combining the DNA coding for the
PT	protein and joining to a plasmid in the bacillus
XX	
PS	Disclosure; Page 19 and Page 32; 38pp; French.
XX	
CC	This sequence comprises a preferred fragment of the Bacillus
CC	amyloliquefaciens alpha-amylase signal sequence fused to a HindIII
CC	linker. The sequence has been compiled from two separate sequences
CC	given in the specification, i.e. the preferred alpha-amylase signal
CC	(Claim 16) and the sequence of the fusion junction (page 19). Plasmid
CC	pKMT52, which contains this construct, is one example of a vector
CC	which is useful for efficient production of proteins in Bacillus
CC	subtilis hosts; the alpha-amylase signal peptide from
CC	B.amyloliquefaciens is 10 x more efficient than that from
CC	B.subtilis. The vector is suitable for increased production of e.g.
CC	antigenic proteins, interferons, pepsin, rennin, etc.
XX	See AAN20145-N20154 and AAN20046.
SQ	Sequence 50 BP; 13 A; 12 C; 10 G; 15 T; 0 other;
	Query Match                      1.8%; Score 19.8; Length 50;
	Best Local Similarity        77.4%; Pred No. 2.5e+04;
	Matches    24; Conservative    0; Mismatches     7; Indels     0; Gaps     0
OY	707 CGATTAGGACGAATCAGCTGCCAAGCTAGC 737
DB	20 CGATTACAAAACATCATCAGCGCAAGCTTGC 50
RESULT 9	
AAAI0655	
XX	AAAI0655 standard; cDNA; 27 BP.
XX	
XX	AAAI0655;
XX	
DT	29-JUN-2000 (first entry)
XX	
DE	PCR primer #9 used in barley VAC screening.
XX	
KM	Rarl; resistance response; pathogen defence; antifungal; barley;
KW	transgenic plant; powdery mildew; increase resistance; gene modification;
XX	PCR primer; yeast artificial chromosome; YAC; ss.
OS	Synthetic.
FN	WO200008160-A2.
XX	
PD	17-FEB-2000.
XX	
PF	06-AUG-1999; 99WO-GB02590.
XX	
PR	06-AUG-1998; 98GB-0017169.
XX	
PA	(PLAN-) PLANT BIOSCIENCE LTD.
XX	
PI	Schulze-Lefert PMJ, Shirsasu K, Lahaye T;
XX	
DR	WPI; 2000-317041/27.
XX	
TT	Novel polynucleotide encoding a Rarl polypeptide from barley, useful

PT for producing transgenic plants with increased pathogen resistance e.g.  
 PT to powdery mildew, and for identifying homologous sequences in other  
 PT species -  
 PS Example 1; Page 98; 131pp; English.

XX This sequence represents a PCR primer used in barley YAC (yeast  
 CC artificial chromosome) screening. The invention relates to barley Rarl  
 CC sequences and to putative homologues of Rarl, OsRarl-h1 (from rice) and  
 CC AtRarl-h1 (from Arabidopsis thaliana). Rarl is a protein involved in the  
 CC barley resistance signalling pathways, and plant pathogen defence  
 CC response signalling pathway. Rarl is required for the action of the R  
 CC (resistance) gene Mla-12. Rarl has antifungal and antifungal  
 CC properties, and functions via gene modification. The Rarl polynucleotides  
 CC are useful in the production of transgenic plants in which a defence  
 CC response is modulated, especially barley with improved resistance to  
 CC pathogens e.g. powdery mildew. They can be used to produce probes and  
 CC primers useful to identify or isolate the polynucleotides (e.g. in a  
 CC plant or plant cell) by standard methods and to isolate Rarl homologues  
 CC from other species, which in turn are useful to manipulate resistance to  
 CC agronomically important diseases. The polypeptides and antibodies raised  
 CC against them are useful to identify and isolate the polypeptides or  
 CC homologous polypeptides e.g. in other species.

SQ Sequence 27 BP; 7 A; 8 C; 6 G; 6 T; 0 other;

Query Match 1.8%; Score 19.6; DB 21; Length 27;  
 Best Local Similarity 84.6%; Pred. No. 2e+04; 4; Indels 0; Gaps 0;  
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 263 GCCCTCTGCTCTACGACGACGACG 238  
 DB 2 GCCCTCTGCTCTACGACGACGACG 27

RESULT 10  
 AAH38571/C  
 ID AAH38571 standard; DNA; 27 BP.

XX AAH38571;  
 AC 14-AUG-2001 (first entry)  
 DE SNP specific SNPE primer SEQ ID 1367.

XX Single nucleotide polymorphism; SNP: single nucleotide primer extension;  
 KW SNPE: genotyping; agammaglobulinaemia; diabetes insipidus; cancer;  
 KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
 KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
 KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
 KW inflammation; forensic investigation; paternity analysis; primer; ss.

XX Homo sapiens.  
 OS  
 XX  
 PN WO200129262-A2.  
 PD 26-APR-2001.  
 PF 13-OCT-2000; 2000WO-US28436.  
 PR 15-OCT-1999; 99US-0160096.  
 PX (ORCHID) ORCHID BIOSCIENCES INC.  
 PA Pileoult-Newburg L, Pohl M;  
 PI  
 XX WPI: 2001-290930/30.

XX New genotyping oligonucleotide, useful for detecting the presence,  
 PT absence or identity of single polynucleotide polymorphism in a nucleic  
 PT acid sample -  
 PS Claim 1; Page 56; 83pp; English.

XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
 CC primer extension (SNPE) primers, and the sequences of regions flanking  
 CC sites of single nucleotide polymorphisms SNPs. The present invention  
 CC includes kits for determining the presence or absence of a SNP, using the  
 CC oligonucleotides of the invention. The PCR primers are used to amplify a  
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
 CC performing a single-nucleotide primer extension reaction. The  
 CC oligonucleotides are useful for determining the presence, absence or  
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
 CC assess by association analysis the genotype of an individual or group of  
 CC individuals, having a pathological phenotype trait suspected of being  
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
 CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
 CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
 CC traits also include symptoms of or susceptibility to multifactorial  
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
 CC inflammation, cancer, nervous system diseases and infection by pathogenic  
 CC microorganism. The method is also useful in forensic investigations and  
 CC paternity analysis. The present sequence represents a single nucleotide  
 CC primer extension (SNPE) primer specific for a human SNP containing DNA  
 CC sequence.

SQ Sequence 27 BP; 5 A; 4 C; 6 G; 11 T; 1 other;

Query Match 1.8%; Score 19.6; DB 22; Length 27;  
 Best Local Similarity 81.5%; Pred. No. 2e+04; 5; Indels 0; Gaps 0;  
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 485 AGAAGCCAAAATATTTGGGTACCA 511  
 DB 27 AGAAGCCAAAATATTTGGGTACCA 1

RESULT 11  
 AAZ68783/C  
 ID AAZ68783 standard; DNA; 47 BP.

XX AAZ68783;  
 AC 10-SEP-2001 (first entry)  
 DE Human map-related diallelic marker SEQ ID NO:3135.

XX Human genome; diallelic marker; high density disequilibrium map;  
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;  
 KW haplotyping; hybridisation; identification; characterisation;  
 KW diagnosis; single nucleotide polymorphism; SNP; ds.

XX Homo sapiens.  
 OS  
 XX  
 FH Key location/Qualifiers  
 FT variation replace(24,C)  
 FT /\*\*tag= a  
 XX /standard\_name= "single nucleotide polymorphism"  
 XX  
 PN WO9954500-A2.  
 PD 28-OCT-1999.  
 PF 21-APR-1999; 99WO-1B00822.  
 PX 21-APR-1998; 98US-0082614.  
 PR 23-NOV-1998; 98US-0109732.  
 PX (GEST ) GENSET.  
 PA Cohen D, Blumenfeld M, Chumakov I;  
 PI  
 XX WPI: 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium  
 PT map of the human genome  
 XX  
 PS Claim 3; Page 899; 2745pp; English.  
 XX  
 CC AA65654 to AA69578 represent human biallelic markers from the present  
 CC invention, which contain a polymorphic base at position 24 of their  
 CC nucleotide sequences. AA69579 to AA277440 represent amplification  
 CC primers for the biallelic markers. The biallelic markers of the  
 CC invention have a variety of uses: they can be used for high density  
 CC mapping of the human genome, and in complex association studies and  
 CC haplotyping studies which are useful in determining the genetic basis  
 CC for disease states. Compositions and methods of the invention can also  
 CC be useful for the identification of the targets for the development of  
 CC pharmaceutical agents and diagnostic methods, as well as the  
 CC characterization of the differential efficacious responses to and side  
 CC effects from pharmaceutical agents acting on a disease as well as other  
 CC treatment.  
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297  
 CC and 3367, are not actually given a sequence in the Sequence Listing  
 CC from the present invention.  
 XX  
 XX Sequence 47 BP; 12 A; 10 C; 17 G; 8 T; 0 other;  
 XX  
 XX Query Match 1.8%; Score 19.6; DB 21; Length 47;  
 XX Best Local Similarity 66.7%; Pred. No. 2.8e+04;  
 XX Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
 OY 903 TGGTTCATCACAAGCATTAACGGCTGCACTCAACTGT 944  
 DB 46 TGGTTCAGCTGAGTCAGCACTCACTCAAGCTGT 5  
 RESULT 12  
 AAT06133/C  
 ID AAT06132 standard; RNA; 47 BP.  
 XX  
 AC AAT06132;  
 XX  
 DT 18-AUG-1997 (first entry)  
 XX  
 DE Substance P binding ligand class 2 consensus sequence.  
 XX  
 KW Ligand; antibody; receptor; SELEX; random library; amplification; PCR;  
 KW Systematic Evolution of Ligands by Exponential enrichment; primer; ss;  
 KW polymerase chain reaction; structure; mimicry; substance P; tachykinin;  
 KW neuropeptide; rheumatoid arthritis; atherosclerosis; cancer;  
 KW diabetic retinopathy.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FH misc\_binding 1..5  
 FT /tag- a  
 FT /note- "binds nucleotides 43-47"  
 FT 13..16  
 FT /tag- b  
 FT /note- "binds nucleotides 35-38"  
 FT 18..30  
 FT /tag- c  
 FT /tag- 35..38  
 FT /tag- d  
 FT /note- "binds nucleotides 13-16"  
 FT 43..47  
 FT /tag- e  
 FT /note- "binds nucleotides 1-5"  
 XX  
 PN WO9530775-A1.  
 XX  
 XX 16-NOV-1995.  
 XX  
 XX 03-MAY-1995; 95WO-US05600.  
 PF

XX  
 PR 21-DEC-1994; 94US-0361795.  
 PR 06-MAY-1994; 94US-0238863.  
 PR 24-MAY-1994; 94US-0248632.  
 PR 09-SEP-1994; 94US-0303362.  
 PR 11-JUN-1990; 90US-0536428.  
 PR 10-JUN-1991; 91US-0714131.  
 PR 21-OCT-1992; 92US-0964624.  
 XX  
 PA (UYRE-) UNIV RES CORP.  
 XX  
 PI Allen P, Doudna JA, Feigon J, Gold L, Nieuwlandt D;  
 PI Schneider DJ, Sullenger BA, Wecker M;  
 XX  
 DR WPI; 1995-404132/51.  
 XX  
 PT Systematic evolution of ligands by exponential enrichment - for  
 PT identifying nucleic acid ligands used in the treatment of, e.g. type  
 PT B insulin resistance and HIV  
 XX  
 PS Example 9; Fig 12B; 209pp; English.  
 XX  
 CC The invention relates to a novel method of isolating ligands that bind  
 CC to target proteins e.g. antibodies or receptors, which bind other  
 CC proteins or ligands. The method, designated Systematic Evolution of  
 CC ligands by Exponential enrichment (SELEX), comprises generating a library  
 CC of random oligonucleotide sequences, about 40-60 nucleotides in length,  
 CC and binding these sequences to the target proteins. After removal of  
 CC unbound material, the remaining bound nucleotide sequences are amplified  
 CC e.g. by PCR, and the newly amplified material is bound again with the  
 CC target protein. This cycle continues until a sufficiently pure  
 CC oligonucleotide sequence is isolated. The method allows the isolation of  
 CC oligonucleotide sequences which structurally mimic the target protein's  
 CC ligand. Ligands AAT06099-130 are examples of nucleic acid ligands which  
 CC bind the tachykinin-family neuropeptide substance P (AAR85243). The new  
 CC ligands were split into 2 groups based on their affinities for substance  
 CC P. Class 1 ligands had binding affinities up to 2 micromolar whereas  
 CC class 2 ligands bound at above 2 micromolar. This sequence represents  
 CC the consensus of the class 2 ligands. The ligands can be used to block  
 CC the activity of substance P and is useful in the treatment of e.g.  
 CC rheumatoid arthritis, atherosclerosis, diabetic retinopathy or cancer.  
 CC  
 SQ Sequence 47 BP; 10 A; 10 C; 10 G; 4 U; 13 other;  
 XX  
 XX Query Match 1.8%; Score 19.4; DB 16; Length 47;  
 XX Best Local Similarity 54.1%; Pred. No. 3.2e+04;  
 XX Matches 20; Conservative 9; Mismatches 8; Indels 0; Gaps 0;  
 OY 357 TGAACATCATCAATTTCACAGTGTGATGCTGAG 393  
 DB 39 TTAACCTGCTCCWDMDWMHMGCTGCTCTTTTTCAG 3  
 RESULT 13  
 AAA07196  
 ID AAA07196 standard; DNA; 42 BP.  
 XX  
 AC AAA07196;  
 XX  
 DT 22-JUN-2000 (first entry)  
 XX  
 DE PCR primer for PHA polymerase gene.  
 XX  
 KW PCR primer; polyhydroxyalkanoate synthesis; thiolate; reductase;  
 KW poly-3-hydroxyalkanoate; PHA synthase; poly-3-hydroxybutyrate;  
 KW PHB synthase; acyl-coenzyme A transferase; enoyl-coenzyme A hydratase;  
 KW biological polyester; biodegradable material;  
 KW biocompatible thermoplastic material; ss.  
 XX  
 OS Pseudomonas oleovorans.  
 XX  
 XX WO200011188-A1.  
 XX  
 XX





CC as well as to examine genetic drift and mutations in plants and to  
 CC detect specific RNA. The ribozymes can be targeted to specific genes or  
 CC to consensus sequences within a family of related genes, and being  
 CC catalytic need to be present at only very low concentrations.

XX Sequence 50 BP; 19 A; 11 C; 11 G; 9 U; 0 other;

Query Match 1.8%; Score 19.2; DB 19; Length 50;  
 Best Local Similarity 47.9%; Pred. No. 3.8e+04;  
 Matches 23; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

OY 723 AGCTGCCAAGCTAGCTACTGACACATCTTGTGGCATCTGCTGGT 770  
 111 111 111 111 111 111 111 111 111 111  
 Db 2 AGCTCAGAGCAACACAGAAACACACCTGUGGACUACUACUCCUGU 49

RESULT 18  
 AAL28793/C  
 AAL28793 standard; DNA; 50 BP.

AAL28793;

24-JAN-2002 (first entry)

Human SNP oligonucleotide #2001.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 XX neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
 XX amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 XX complement related protein; cytochrome; kinesin; cytokine; interferon;  
 XX interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 XX multifactorial disease; autoimmune disease; infection;  
 XX nervous system disease; ss.

XX Homo sapiens.

XX WO200147944-A2.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US35498.

XX 28-DEC-1999; 99US-0173419.

XX 27-DEC-2000; 2000US-0173419.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI; 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 XX oncogenes and histones, useful for diagnosing and treating, e.g.  
 XX cancer, autoimmune diseases and infections.

XX Claim 1; Page 1953; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic  
 XX variants of proteins related to amylases, cyclin, polymerase, oncogenes,  
 XX apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
 XX histones, kinases, colony stimulating factors, complement related  
 XX proteins, cytochromes, kinesins, cytokines, interferons, interleukins,  
 XX G-protein coupled receptors and thioesterases. The present sequence is  
 XX one such oligonucleotide. The oligonucleotides and the peptides encoded  
 XX by them may be used in the prevention, diagnosis and treatment of  
 XX diseases associated with inappropriate expression of the proteins listed  
 XX above. Disorders that may be prevented, diagnosed and/or treated include  
 XX multifactorial diseases with a genetic component, such as autoimmune  
 XX diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
 XX systemic lupus erythematosus and Grave's disease), inflammation, cancer  
 XX (e.g. cancers of the bladder, brain, breast, colon and kidney, pathogenic  
 XX leukemia), diseases of the nervous system and an infection of pathogenic

CC organisms.

XX Sequence 50 BP; 17 A; 13 C; 13 G; 7 T; 0 other;

SO Query Match 1.8%; Score 19.2; DB 22; Length 50;  
 Best Local Similarity 67.5%; Pred. No. 3.8e+04;  
 Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 46 CCTTTGACTCTGAGCTTCCCGAACCCTGCTGATTTTG 85  
 111 111 111 111 111 111 111 111 111 111  
 Db 40 CCAGCTGATTTTGGTTCCAGACCCCAATGATTTTG 1

RESULT 19  
 AAD08176/C  
 ID AAD08176 standard; DNA; 35 BP.

XX AAD08176;

XX 07-AUG-2001 (first entry)

XX Murine prostate stem cell antigen cDNA amplifying sense PCR primer.

XX Murine; prostate stem cell antigen; PSCA; cytostatic; gene therapy;  
 XX glycoprotein; cancer; prostate; bladder; lung; tumour; PCR primer; ss.

XX Mus musculus.

XX WO200140309-A2.

XX 07-JUN-2001.

XX 27-OCT-2000; 2000WO-US29603.

XX 29-OCT-1999; 99US-0162558.

XX 16-FEB-2000; 2000US-0182872.

XX (GENTH ) GENTECH INC.

XX Devaux B, Keller G, Koepfen H, Lasky LA;

XX WPI; 2001-389954/41.

XX Novel anti-prostate stem cell antigen (PSCA) antibody that internalizes  
 XX on binding to PSCA on mammalian cell and inhibits growth of  
 XX PSCA-expressing cancer cells in vivo, useful for killing  
 XX PSCA-expressing cancer cells.

XX Example 12; Page 71; 112pp; English.

XX The present sequence is a PCR primer used for amplifying murine  
 XX prostate stem cell antigen (PSCA) cDNA. PSCA is a single subunit  
 XX glycoprotein that is expressed on the cell surface as a  
 XX glycosylphosphatidylinositol (GPI)-anchored protein. The present  
 XX invention relates to anti-PSCA antibody composition and methods of  
 XX killing PSCA-expressing cancer cells. PSCA is useful for inhibiting and  
 XX killing the growth of PSCA-expressing cancer cells such as prostate  
 XX cancer, bladder cancer or lung cancer cells. Humanised antibody  
 XX conjugated to a toxin or a radioactive isotope is used for killing the  
 XX cancer cells. PSCA is useful for specifically targeting PSCA-expressing  
 XX tumour cells in vivo and for inhibiting or killing these cells. The  
 XX antibodies are also useful for treating the above mentioned cancers and  
 XX for diagnosing and staging of PSCA-expressing cancer, for purification  
 XX or immunoprecipitation of PSCA from cells, and for detection and  
 XX quantitation of PSCA in vitro. PSCA DNA is also useful for treating  
 XX cancers by gene therapy techniques.

XX Sequence 35 BP; 9 A; 11 C; 5 G; 10 T; 0 other;

SO Query Match 1.7%; Score 19; DB 22; Length 35;  
 Best Local Similarity 71.4%; Pred. No. 3.6e+04;  
 Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 707 CGATTAGCAAGAAATCAGCTGCCAGCTAGTACT 741  
 DB 35 CGATTGTGAAGGATGAGCTGCAAAAGCTTCATAGT 1

RESULT 20  
 AA249438  
 ID AA249438 standard; DNA; 37 BP.  
 AC AA249438;  
 XX  
 XX  
 DT 04-APR-2000 (first entry)  
 XX  
 XX  
 DE PCR primer MJ-rele/1CWM for amplification of M. jannaschli rele gene.  
 XX  
 XX  
 KW PCR primer: MJ-rele/1CWM; rele gene; plasmid pNDM220; plasmid PHA705;  
 KW E. coli K-12 strain MC1000; ss.  
 XX  
 XX  
 OS Methanococcus jannaschli.  
 OS Synthetic.  
 XX  
 XX  
 PD W0958652-A2.  
 XX  
 PD 18-NOV-1999.  
 XX  
 XX  
 PF 07-MAY-1999; 99WO-DK00258.  
 XX  
 XX  
 PR 07-MAY-1998; 98DK-0000627.  
 PR 12-MAY-1998; 98US-0085067.  
 XX  
 PA (GXBI-) GX BIOSYSTEMS AS.  
 PI Gerdes K, Gøtfredsen M, Gronlund H, Pedersen K, Kristoffersen P;  
 XX  
 DR WPI; 2000-126366/11.  
 XX  
 PT Novel cytotoxin-based biological containment used to conditionally  
 PT control the survivability of a recombinant cell  
 XX  
 XX  
 PS Example 9; Page 58; 127pp; English.  
 CC  
 CC The present sequence is PCR primer MJ-rele/1CWM for amplification of  
 CC rele gene. The resulting fragment was cloned into plasmid pNDM220  
 CC yielding PHA705. The plasmid is transformed into E. coli K-12 strain  
 CC MC1000. This demonstrates that M. jannaschli Rele is toxic to E. coli.  
 CC  
 XX  
 SQ Sequence 37 BP; 8 A; 10 C; 12 G; 7 T; 0 other;

Query Match 1.7%; Score 19; DB 21; Length 37;  
 Best Local Similarity 81.5%; Pred. No. 3.7e+04;  
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 108 CCAGATCGAAGCTTTGAAGAAGTTGG 134  
 DB 11 CGAGCTCGAGGCTTTGAAGAAGATTGG 37

RESULT 21  
 ABL31957  
 ID ABL31957 standard; DNA; 45 BP.  
 AC ABL31957;  
 XX  
 XX  
 DT 22-MAR-2002 (first entry)  
 XX  
 XX  
 DE PVUII/FokI loop containing primer.  
 XX  
 XX  
 KW Genetic analysis; sequence variant detection; genotype; APOE; SNP;  
 KW single nucleotide polymorphism; polymorphic site; atherosclerosis;  
 KW dementia; Parkinson's disease; Huntington's disease; PCR primer;  
 KW neurodegenerative disease; ss.  
 XX  
 XX  
 OS Synthetic.

XX  
 PN W0200190419-A2.  
 XX  
 PD 29-NOV-2001.  
 XX  
 XX  
 PF 23-MAY-2001; 2001WO-US16577.  
 XX  
 XX  
 PR 23-MAY-2000; 2000US-206613P.  
 PR 23-OCT-2000; 2000US-0696998.  
 PR 25-OCT-2000; 2000US-0697013.  
 PR 25-OCT-2000; 2000US-0697028.  
 XX  
 PA (VARI-) VARIAGENICS INC.  
 PA (STAN/) STANTON V P.  
 XX  
 PI Stanton VP;  
 XX  
 DR WPI; 2002-097670/13.  
 XX  
 XX  
 PT Determining the haplotype of at least one allele of a selected gene at  
 PT two or more polymorphic sites, for assessing disease risk, comprises  
 PT allele-specific enrichment, optical mapping, or atomic force microscopy

Disclosure; Fig 6; 166pp; English.

CC The present invention describes a method for determining the haplotype  
 CC of an allele of a selected gene at two or more polymorphic sites  
 CC comprising allele-specific enrichment, optical mapping, or atomic force  
 CC microscopy. The method is useful for genetic analysis when the DNA  
 CC segment being haplotyped consists of polymorphisms that are in some  
 CC degree of linkage disequilibrium with each other, that is they do not  
 CC assort randomly in the population being studied. The method allows early  
 CC implementation of preventive measures in patients at risk of diseases  
 CC such as atherosclerosis, dementia, Parkinson's disease, Huntington's  
 CC disease or other organic or vascular neurodegenerative diseases. Genotype  
 CC and haplotype information can be used to make diagnostic tests useful for  
 CC disease risk assessment, for prognostic prediction of the course or  
 CC outcome of a disease, to diagnose a disease or condition, or to select  
 CC an optimal therapy for a disease or condition. ABL31915 to ABL32035  
 CC represent nucleotide sequence used in the exemplification of the present  
 CC invention.

XX  
 SQ Sequence 45 BP; 12 A; 8 C; 15 G; 10 T; 0 other;

Query Match 1.7%; Score 19; DB 24; Length 45;  
 Best Local Similarity 71.4%; Pred. No. 4.2e+04;  
 Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 269 TTGCTTAGCAAGGAGCAGCTTGGGATGATCT 303  
 DB 10 TTGCGCTAGCAAGACCAAGACAGCTGATGATTT 44

RESULT 22  
 AAV03973/C  
 ID AAV03973 standard; DNA; 47 BP.  
 AC AAV03973;  
 XX  
 XX  
 DT 22-MAY-1998 (first entry)  
 XX  
 XX  
 DE LDR probe SODEX-3-12R.  
 XX  
 XX  
 KW Detection; single-base change; insertion; deletion; translocation;  
 KW probe; ligation detection reaction; LDR; PCR; ss.  
 XX  
 XX  
 OS Synthetic.  
 OS W09745559-A1.  
 XX  
 XX  
 PD 04-DEC-1997.  
 XX

```

PF 27-MAY-1997; 97WO-US09012.
XX
PR 29-MAY-1996; 96US-0018532.
XX
PA (CORR ) CORNELL RES FOUND INC.
XX
PI Barany F, Belgrader P, Lubin M;
XX
DR WPI; 1998-032663/03.
XX
PT Multiplex detection of nucleic acid sequence differences - using
XX lligase detection reaction coupled to PCR, useful for determining
XX gene dosage, for detecting genetic disorders, etc.
XX
PS Example 2; Page 72; 158pp; English.
XX
CC The present sequence was used in the development of three novel
XX methods for the detection nucleic acid sequence differences, i.e.
XX single-base changes, insertions, deletions or translocations. The
XX 1st uses the lligase detection reaction (LDR) coupled to PCR, the
XX 2nd a 1st PCR coupled to a 2nd PCR coupled to a LDR and the 3rd a
XX 1st PCR coupled to a 2nd PCR.
XX
CC Sequence 47 BP; 11 A; 12 C; 14 G; 10 T; 0 other;
XX
Query Match 1.7%; Score 19; DB 19; Length 47;
Best Local Similarity 65.1%; Pred. No. 4.3e+04;
Matches 28; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 614 ATCACAGCTATGCAATGTCCTCCAGTTTGGATGA 656
DB 44 AACTACCGCACTATGAGCGCCACCGTCTTTCTGCATAGA 2
RESULT 23
AAZ69509/C
ID AAZ69509 standard; DNA; 47 BP.
XX
AC AAZ69509;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human map-related biallelic marker SEQ ID NO:3865.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
XX genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX haplotyping; hybridisation; identification; characterisation;
XX diagnosis; single nucleotide polymorphism; SNP; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX variation /tag= a
XX /standard_name= "single nucleotide polymorphism"
XX
PN WO954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB00822.
XX
PR 21-APR-1998; 98US-0082614.
XX
PR 23-NOV-1998; 98US-0109732.
XX
XX (GENT ) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX
XX WPI; 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome

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XX
PS Claim 3; Page 1055; 2745pp; English.
XX
XX AAZ69578 represent human biallelic markers from the present
XX invention, which contain a polymorphic base at position 24 of their
XX nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
XX primers for the biallelic markers. The biallelic markers of the
XX invention have a variety of uses: they can be used for high density
XX mapping of the human genome, and in complex association studies and
XX for disease studies. Compositions and methods of the invention can also
XX be useful for the identification of the targets for the development of
XX pharmaceutical agents and diagnostic methods, as well as the
XX characterisation of the differential efficacious responses to and side
XX effects from pharmaceutical agents acting on a disease as well as other
XX treatment.
XX
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
XX and 3367, are not actually given a sequence in the Sequence Listing
XX from the present invention.
XX
S0 Sequence 47 BP; 19 A; 9 C; 3 G; 16 T; 0 other;
XX
Query Match 1.7%; Score 19; DB 21; Length 47;
Best Local Similarity 65.1%; Pred. No. 4.3e+04;
Matches 28; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 961 ATAGAGAAATATGACTATCCCGGGGAGAGATGTCATGTGTG 1003
DB 43 AGATATTATATGCAATTTGTGTGTAATATTCATCATGTATTG 1
RESULT 24
AAV40515
ID AAV40515 standard; cDNA; 29 BP.
XX
AC AAV40515;
XX
DT 09-NOV-1998 (first entry)
XX
DE Human secreted protein DF518_3 gene probe.
XX
KW Secreted protein; DF518_3; human; probe; ss.
XX
XX Synthetic.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 2 /tag= a
XX /note= "biotinylated phosphoramidite residue"
XX
XX WO9830582-A2.
XX
PD 16-JUL-1998.
XX
PF 09-JAN-1998; 98WO-US00289.
XX
PR 08-JAN-1998; 98US-0004680.
XX
PR 09-JAN-1997; 97US-0780890.
XX
XX (GENT ) GENETICS INST INC.
XX
XX Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
XX Racie LA, Spaulding V, Treacy M;
XX
XX WPI; 1998-413681/35.
XX
XX New isolated nucleic acids and secreted proteins - obtained from
XX human foetal kidney, human adult retina, human foetal brain, human
XX adult brain and human adult blood cDNA libraries
XX
PS Disclosure; Page 84; 103pp; English.

```



CC This biotinylated oligonucleotide was designed for use as a  
 CC probe to isolate full-length DF518.3 (see AAV40506) sequences. This  
 CC clone, deposited at ATCC 98290, codes for a novel human secreted  
 CC protein (see AAW29653), and was originally isolated from a human  
 CC adult brain cDNA library. The invention relates to 9 cDNA clones  
 CC (see AAV40501-09) which code for human secreted proteins (see  
 CC AAW29648-56) of the foetal kidney or brain, or adult brain, retina  
 CC or blood, that may have a variety of potential activities.  
 XX

SQ Sequence 29 BP; 5 A; 5 C; 7 G; 11 T; 1 other;

Query Match Best Local Similarity 1.7%; Score 18.8; DB 19; Length 29;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 977 TCCTGGGAGGATGTCATGT 998

Db 7 TCCTGGTGAAGATGTCATGT 28

RESULT 25

AAH23347 standard: DNA; 34 BP.

AAH23347;

17-SEP-2001 (first entry)

Nucleotide sequence of primer BCF3L12.

Nucleic acid binding polypeptide; repressor domain; cardiant; nootropic;

circulatory active; anti-inflammatory; dermatological; neuroprotective;

cerebroprotective; antibacterial; antifungal; antiviral; antirheumatic;

osteopathic; gene therapy; zinc finger; binding site; PCR primer; SS.

Synthetic.

WO200153480-A1.

26-JUL-2001.

19-JAN-2001; 2001WO-GB00202.

24-JAN-2000; 2000GB-0001582.

30-MAY-2000; 2000GB-0013102.

30-MAY-2000; 2000GB-0013103.

30-MAY-2000; 2000GB-0013104.

(GEND-) GENDAO LTD.

Choo Y, Kling A, Moore M;

WPI: 2001-451906/48.

Nucleic acid binding polypeptide, used to identify nucleic acids and  
 treat inflammatory, neurological, and dermatological disease, comprises  
 a repressor domain and several nucleic acid binding domains linked by  
 non-canonical linker(s) -

Example 25; Page 92; 142pp; English.

The invention relates to a nucleic acid (NA) binding polypeptide (I)  
 comprising a repressor domain and several NA binding domains (BDs) linked  
 by at least one non-canonical linker. (I) may be used to identify NAs in  
 a complex mixture, to differentiate single base pair changes in NAs, in  
 the manufacture of chimeric restriction enzymes, to produce knock out  
 organisms, and in the treatment of diseases such as: cardiovascular,  
 inflammatory, metabolic, infectious, neurological, rheumatological,  
 genetic, dermatological, and musculoskeletal diseases. The invented  
 methods are used to produce novel NA binding polynucleotides and to  
 modify existing NA binding polynucleotides comprising several NA BDs.  
 The novel polypeptide comprises several nucleic acid binding domains  
 linked by linker sequences. The invented polypeptide is therefore able

CC to span longer or variable gaps, and a greater number of gaps, between  
 CC DNA binding substrates. Sequences AAH23338-357 represent PCR primers  
 CC used in the course of the invention.  
 XX

SQ Sequence 34 BP; 4 A; 7 C; 10 G; 13 T; 0 other;

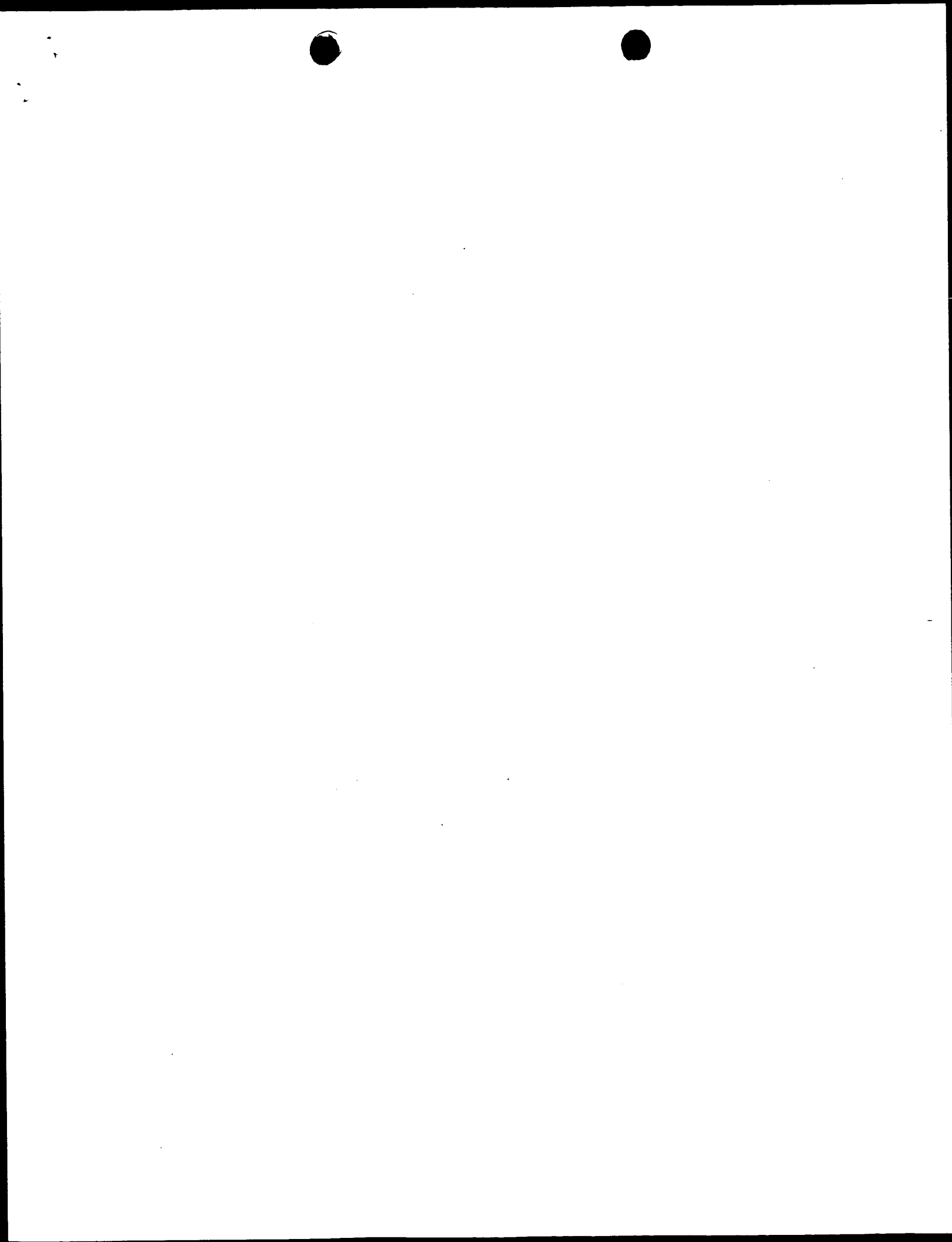
Query Match Best Local Similarity 1.7%; Score 18.8; DB 22; Length 34;

Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 634 GTCCCTCCAGGTTTGGATGATGTTGGT 663

Db 4 GTCCCTCCAGGATGATGATGATGTTGGT 33

Search completed: October 22, 2002, 15:48:24  
 Job time : 209 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: October 22, 2002, 15:30:26 : Search time 48 Seconds

(without alignments)  
5357.458 Million cell updates/sec

Title: US-09-374-967-1

Perfect score: 1086

Sequence: 1 atgaagcccatcttctgt.....agcctgagatcgtcatgtga 1086

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 389450

Minimum DB seq length: 20

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Issued\_Patents\_NA: \*  
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4: /cgn2\_6/ptodata/2/1na/6B.COMB.seq: \*  
5: /cgn2\_6/ptodata/2/1na/PCrus.COMB.seq: \*  
6: /cgn2\_6/ptodata/2/1na/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	21.2	2.0	42	1	US-08-660-626-13
2	21.2	2.0	42	3	US-09-031-168-13
3	20.6	1.9	45	2	US-08-860-882A-8
4	20.2	1.9	45	1	US-08-483-415-29
5	20.2	1.9	45	6	5487983-26
6	20.2	1.9	50	3	US-08-985-162-1708
7	19.4	1.8	47	1	US-08-441-591-60
8	19.4	1.8	47	1	US-08-303-362A-60
9	19.4	1.8	47	5	PCT-US95-05600-77
10	19.2	1.8	48	1	US-08-009-265-19
11	19.2	1.8	48	5	PCT-US94-06079-40
12	19.2	1.8	47	3	US-08-864-473-10
13	19.2	1.8	47	3	US-08-864-473-10
14	19.2	1.8	47	3	US-08-864-473-10
15	18.8	1.7	50	4	US-09-440-523-10
16	18.8	1.7	50	4	US-08-998-099-298
17	18.6	1.7	28	4	US-09-042-943-13
18	18.6	1.7	34	1	US-08-437-841-28
19	18.6	1.7	34	1	US-08-286-521-28
20	18.6	1.7	34	1	US-08-436-175-28
21	18.6	1.7	34	5	US-08-943-682-28
22	18.6	1.7	45	3	PCT-US95-09464-28
23	18.6	1.7	45	3	US-08-406-855A-9
24	18.6	1.7	50	2	US-09-206-899-9
25	18.6	1.7	50	3	US-08-715-568A-6
26	18.2	1.7	50	3	US-08-985-162-1663
27	18.2	1.7	40	4	US-09-153-310-19
28	18.2	1.7	42	1	US-08-303-124-25

28	18.2	1.7	42	2	US-08-480-697B-25	Sequence 25, Appl
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31	18.2	1.7	50	3	US-08-998-099-321	Sequence 321, Ap
32	18.2	1.7	45	1	US-08-171-389-34	Sequence 34, Appl
33	18.2	1.7	45	1	US-08-123-936-34	Sequence 34, Appl
34	18.2	1.7	45	2	US-08-475-228A-34	Sequence 34, Appl
35	18.2	1.7	45	2	US-08-482-080A-415	Sequence 415, App
36	18.2	1.7	45	5	PCT-US93-12388-34	Sequence 34, Appl
37	18.2	1.7	50	1	US-08-171-389-415	Sequence 34, Appl
38	18.2	1.7	50	1	US-08-123-936-415	Sequence 415, App
39	18.2	1.7	50	2	US-08-475-228A-415	Sequence 415, App
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41	18.2	1.7	30	1	US-08-410-739-1	Sequence 1, Appl
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44	18.2	1.7	30	2	US-08-569-806-18	Sequence 18, Appl
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53	18.2	1.7	44	3	US-08-463-682-15	Sequence 70, Appl
54	18.2	1.7	44	3	US-08-171-389-255	Sequence 15, Appl
55	18.2	1.7	46	1	US-08-123-936-255	Sequence 255, Appl
56	18.2	1.7	46	2	US-08-475-228A-255	Sequence 255, Appl
57	18.2	1.7	46	3	US-08-482-080A-255	Sequence 255, App
58	18.2	1.7	46	5	PCT-US93-12388-255	Sequence 255, App
59	18.2	1.7	50	4	US-09-315-886C-4	Sequence 255, App
60	18.2	1.7	50	5	PCT-US94-01183-14	Sequence 4, Appl
61	18.2	1.7	33	1	US-08-138-608-14	Sequence 14, Appl
62	18.2	1.7	41	3	US-08-813-507-75	Sequence 75, Appl
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65	18.2	1.7	43	1	US-07-714-131C-335	Sequence 335, App
66	18.2	1.7	43	1	US-08-412-110-335	Sequence 335, App
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87	18.2	1.7	34	2	US-08-739-158-86	Sequence 86, Appl
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97	18.2	1.7	34	2	US-08-739-158-86	Sequence 86, Appl
98	18.2	1.7	34	2	US-08-739-158-86	Sequence 86, Appl
99	18.2	1.7	34	2	US-08-739-158-86	Sequence 86, Appl
100	18.2	1.7	34	2	US-08-739-158-86	Sequence 86, Appl

101	17.2	1.6	47	4	US-09-218-207-328	Sequence 328, App	174	16.6	1.5	33	3	US-09-073-259-15	Sequence 15, Appl
102	17.2	1.6	48	1	US-08-472-194A-25	Sequence 25, Appl	175	16.6	1.5	33	4	US-09-363-095-15	Sequence 15, Appl
103	17.2	1.6	48	3	US-09-262-142-25	Sequence 25, Appl	176	16.6	1.5	33	4	US-09-418-027-15	Sequence 15, Appl
104	17.2	1.6	48	4	US-08-849-567A-25	Sequence 25, Appl	177	16.6	1.5	36	1	US-08-291-932A-197	Sequence 197, App
105	17.2	1.6	50	2	US-08-867-579-1	Sequence 1, Appl1	178	16.6	1.5	36	2	US-08-795-006A-18	Sequence 26, App
106	17.2	1.6	50	3	US-08-985-162-1649	Sequence 1649, Ap	179	16.6	1.5	36	2	US-08-961-083-296	Sequence 18, Appl
107	17.2	1.6	50	3	US-08-985-162-1749	Sequence 1749, Ap	180	16.6	1.5	36	4	US-09-184-073-18	Sequence 3, Appl1
108	17.2	1.6	50	3	US-08-985-162-1758	Sequence 1758, Ap	181	16.6	1.5	38	1	US-07-720-585A-3	Sequence 5, Appl1
109	17	1.6	27	4	US-08-584-040-3334	Sequence 3334, Ap	182	16.6	1.5	40	1	US-08-178-014A-5	Sequence 5, Appl1
110	17	1.6	30	5	PCT-US91-06234A-8	Sequence 8, Appl1	183	16.6	1.5	40	1	US-08-679-493A-89	Sequence 89, Appl
111	17	1.6	30	6	5212256-15	Patent No. 5212296	184	16.6	1.5	45	4	US-07-741-940-26	Sequence 26, Appl
112	17	1.6	45	1	US-08-105-483-99	Sequence 99, Appl	185	16.6	1.5	46	1	US-08-289-548A-26	Sequence 26, Appl
113	17	1.6	45	1	US-08-709-209-99	Sequence 99, Appl	186	16.6	1.5	46	1	US-08-452-654-26	Sequence 26, Appl
114	17	1.6	45	1	US-08-458-101-99	Sequence 99, Appl	187	16.6	1.5	46	1	US-08-452-654B-26	Sequence 26, Appl
115	17	1.6	45	1	US-08-358-627F-2	Sequence 2, Appl1	188	16.6	1.5	46	3	US-08-450-582-26	Sequence 168, App
116	17	1.6	48	1	US-08-049-473-17	Sequence 17, Appl	189	16.6	1.5	46	3	US-08-172-389-168	Sequence 19, Appl
117	17	1.6	48	1	US-08-312-648-17	Sequence 17, Appl	190	16.6	1.5	47	1	US-08-104-072B-19	Sequence 168, App
118	17	1.6	48	5	PCT-US94-04190-17	Sequence 17, Appl	191	16.6	1.5	47	1	US-08-123-93B-168	Sequence 168, App
119	17	1.6	49	1	US-08-155-171B-28	Sequence 28, Appl	192	16.6	1.5	47	1	US-08-475-228A-168	Sequence 168, App
120	17	1.6	49	2	US-08-435-998-28	Sequence 28, Appl	193	16.6	1.5	47	3	US-08-482-080A-168	Sequence 268, App
121	17	1.6	50	1	US-08-207-901-103	Sequence 103, App	194	16.6	1.5	47	4	US-09-338-907-268	Sequence 168, App
122	17	1.6	50	3	US-08-985-162-1662	Sequence 1662, App	195	16.6	1.5	47	5	PCT-US93-12388-168	Sequence 12, Appl
123	17	1.6	50	3	US-08-985-162-1669	Sequence 1669, App	196	16.6	1.5	48	1	US-08-555-268A-12	Sequence 12, Appl
124	17	1.6	50	3	US-08-985-162-1670	Sequence 1670, App	197	16.6	1.5	48	2	US-08-495-695B-12	Sequence 12, Appl
125	17	1.6	50	3	US-08-985-162-1677	Sequence 1677, App	198	16.6	1.5	48	5	PCT-US94-14436-12	Sequence 35, Appl
126	17	1.6	50	3	US-08-985-162-1682	Sequence 1682, App	199	16.6	1.5	49	1	US-08-476-008-35	Sequence 35, Appl
127	17	1.6	50	3	US-08-985-162-1683	Sequence 1683, App	200	16.6	1.5	49	1	US-08-306-063-35	Sequence 35, Appl
128	17	1.6	50	3	US-08-985-162-1693	Sequence 1693, App	201	16.6	1.5	49	1	US-08-833-485-35	Sequence 35, Appl
129	17	1.6	50	3	US-08-985-162-1698	Sequence 1698, App	202	16.6	1.5	49	1	US-08-833-485-35	Sequence 35, Appl
130	17	1.6	50	3	US-08-985-162-1717	Sequence 1717, App	203	16.6	1.5	49	1	US-08-833-485-35	Sequence 35, Appl
131	17	1.6	50	3	US-08-985-162-1719	Sequence 1719, App	204	16.6	1.5	49	4	US-09-137-440-35	Sequence 35, Appl
132	17	1.6	50	3	US-08-985-162-1729	Sequence 1729, App	205	16.6	1.5	49	4	US-09-115-488-3	Sequence 35, Appl
133	17	1.6	50	3	US-08-985-162-1751	Sequence 1751, App	206	16.6	1.5	50	1	PCT-US91-06148A-35	Sequence 35, Appl
134	17	1.6	50	3	US-08-985-162-1754	Sequence 1754, App	207	16.6	1.5	50	1	US-08-513-764-3	Sequence 35, Appl
135	17	1.6	50	3	US-08-985-162-1756	Sequence 1756, App	208	16.6	1.5	50	3	US-08-985-162-1696	Sequence 1696, App
136	17	1.6	50	3	US-08-998-099-293	Sequence 293, App	209	16.6	1.5	50	3	US-08-985-162-1758	Sequence 1728, App
137	17	1.6	50	3	US-08-998-099-301	Sequence 301, App	210	16.6	1.5	50	3	US-08-998-099-307	Sequence 307, App
138	17	1.6	50	3	US-08-998-099-304	Sequence 304, App	211	16.6	1.5	50	3	US-08-998-099-307	Sequence 307, App
139	17	1.6	50	3	US-08-998-099-309	Sequence 309, App	212	16.6	1.5	50	3	US-08-584-040-4888	Sequence 4888, App
140	17	1.6	50	3	US-08-998-099-315	Sequence 315, App	213	16.6	1.5	50	3	US-09-115-488-3	Sequence 35, Appl1
141	16.8	1.5	24	2	US-08-705-625-8	Sequence 8, Appl1	214	16.4	1.5	28	4	US-09-115-488-3	Sequence 35, Appl1
142	16.8	1.5	24	2	US-09-220-574-8	Sequence 8, Appl1	215	16.4	1.5	27	4	US-08-886-886-35	Sequence 35, Appl1
143	16.8	1.5	26	1	US-08-499-568-6	Sequence 6, Appl1	216	16.4	1.5	36	2	US-08-417-495-15	Sequence 15, Appl
144	16.8	1.5	26	1	US-08-793-958-6	Sequence 6, Appl1	217	16.4	1.5	36	2	US-08-284-991B-15	Sequence 15, Appl
145	16.8	1.5	29	4	US-09-359-361-4	Sequence 4, Appl1	218	16.4	1.5	36	3	US-08-778-487-14	Sequence 14, Appl
146	16.8	1.5	33	1	US-08-449-207-1	Sequence 1, Appl1	219	16.4	1.5	36	3	US-08-891-516-14	Sequence 14, Appl
147	16.8	1.5	33	1	US-08-449-207-1	Sequence 1, Appl1	220	16.4	1.5	36	3	US-08-952-948-3	Sequence 3, Appl1
148	16.8	1.5	34	4	US-08-250-802-30	Sequence 30, Appl	221	16.4	1.5	36	3	US-08-952-948-3	Sequence 3, Appl1
149	16.8	1.5	34	5	PCT-US92-07916-30	Sequence 30, Appl	222	16.4	1.5	36	5	PCT-US92-01785-15	Sequence 15, Appl
150	16.8	1.5	36	4	US-09-101-126-13	Sequence 13, Appl	223	16.4	1.5	36	5	PCT-US92-01785-15	Sequence 15, Appl
151	16.8	1.5	36	4	US-09-026-276-9	Sequence 9, Appl1	224	16.4	1.5	36	5	PCT-US92-01785-15	Sequence 15, Appl
152	16.8	1.5	40	2	US-08-584-760A-56	Sequence 56, Appl	225	16.4	1.5	38	1	US-08-180-195-6	Sequence 6, Appl1
153	16.8	1.5	42	2	US-08-280-864A-1	Sequence 1, Appl1	226	16.4	1.5	38	1	US-08-180-195-6	Sequence 6, Appl1
154	16.8	1.5	42	2	US-08-250-802-31	Sequence 31, Appl	227	16.4	1.5	38	1	US-08-477-329-7	Sequence 7, Appl1
155	16.8	1.5	42	4	US-09-092-291-1	Sequence 1, Appl1	228	16.4	1.5	38	2	US-08-475-458-6	Sequence 6, Appl1
156	16.8	1.5	42	5	PCT-US92-07916-31	Sequence 31, Appl	229	16.4	1.5	38	2	US-08-475-458-6	Sequence 6, Appl1
157	16.8	1.5	43	5	PCT-US95-09458-1	Sequence 1, Appl1	230	16.4	1.5	38	3	US-08-980-400-6	Sequence 6, Appl1
158	16.8	1.5	43	5	US-08-109-037-22	Sequence 22, Appl	231	16.4	1.5	38	3	US-08-980-400-6	Sequence 6, Appl1
159	16.8	1.5	43	3	US-08-109-037-55	Sequence 55, Appl	232	16.4	1.5	38	3	US-08-980-400-6	Sequence 6, Appl1
160	16.8	1.5	43	3	US-08-109-037-56	Sequence 56, Appl	233	16.4	1.5	38	4	US-09-583-459A-7	Sequence 7, Appl1
161	16.8	1.5	43	3	US-08-109-037-57	Sequence 57, Appl	234	16.4	1.5	38	4	US-09-583-459A-7	Sequence 7, Appl1
162	16.8	1.5	44	1	US-08-121-202-18	Sequence 18, Appl	235	16.4	1.5	38	4	US-09-583-459A-7	Sequence 7, Appl1
163	16.8	1.5	44	5	PCT-US93-11638-12	Sequence 12, Appl	236	16.4	1.5	38	4	US-09-583-459A-7	Sequence 7, Appl1
164	16.8	1.5	46	3	US-08-463-682-13	Sequence 13, Appl	237	16.4	1.5	38	4	US-09-583-459A-7	Sequence 7, Appl1
165	16.8	1.5	48	2	US-08-697-404-2	Sequence 2, Appl1	238	16.4	1.5	38	4	US-09-583-459A-7	Sequence 7, Appl1
166	16.8	1.5	49	2	US-08-595-043A-62	Sequence 62, Appl	239	16.4	1.5	40	2	US-08-463-685-19	Sequence 19, Appl
167	16.6	1.5	23	3	US-08-985-908-28	Sequence 28, Appl	240	16.4	1.5	40	2	US-07-965-285-19	Sequence 19, Appl
168	16.6	1.5	31	1	US-08-019-870-33	Sequence 33, Appl	241	16.4	1.5	40	4	US-08-467-231-19	Sequence 19, Appl
169	16.6	1.5	31	1	US-08-214-580A-3	Sequence 3, Appl1	242	16.4	1.5	40	4	US-09-201-912-19	Sequence 19, Appl
170	16.6	1.5	31	1	US-09-052-689-7	Sequence 7, Appl1	243	16.4	1.5	40	4	US-09-358-972-211	Sequence 211, Appl
171	16.6	1.5	31	4	US-08-992-877-66	Sequence 66, Appl	244	16.4	1.5	40	4	US-09-406-064-17	Sequence 47, Appl
172	16.6	1.5	33	3	US-09-073-354-15	Sequence 15, Appl	245	16.4	1.5	40	4	US-09-430-615-47	Sequence 52, Appl
173	16.6	1.5	33	3	US-08-656-005A-15	Sequence 15, Appl	246	16.4	1.5	41	2	US-08-190-199A-26	Sequence 26, Appl

247	16.4	1.5	44	2	US-08-749-852-5	Sequence 5, Appl	C 320	16	1.5	27	4	US-08-584-040-3464	Sequence 3464, Ap
C 248	16.4	1.5	44	1	US-09-201-075-3	Sequence 3, Appl	C 321	16	1.5	28	4	US-09-098-628-12	Sequence 12, Appl
C 249	16.4	1.5	45	1	US-08-486-137-3	Sequence 3, Appl	C 322	16	1.5	28	5	PCT-US91-02186-16	Sequence 16, Appl
C 250	16.4	1.5	45	1	US-08-485-180-3	Sequence 3, Appl	C 323	16	1.5	28	5	US-08-384-708A-16	Sequence 180, App
C 251	16.4	1.5	45	1	US-08-537-002A-14	Sequence 3, Appl	C 324	16	1.5	30	1	US-08-096-623A-94	Sequence 94, Appl
C 252	16.4	1.5	45	1	US-08-419-765-3	Sequence 3, Appl	C 325	16	1.5	30	1	US-08-687-421-180	Sequence 11, Appl
C 253	16.4	1.5	45	3	US-08-863-010-14	Sequence 14, Appl	C 326	16	1.5	30	3	US-08-687-421-180	Sequence 11, Appl
C 254	16.4	1.5	45	3	US-08-863-010-14	Sequence 14, Appl	C 327	16	1.5	31	4	US-08-026-143B-25	Sequence 25, Appl
C 255	16.4	1.5	45	6	US-09-024-429-14	Sequence 14, Appl	C 328	16	1.5	31	5	PCT-US92-10623-25	Sequence 25, Appl
C 256	16.4	1.5	47	4	US-09-338-907-266	Sequence 266, App	C 329	16	1.5	31	5	PCT-US94-02233-25	Sequence 25, Appl
C 257	16.4	1.5	47	4	US-09-218-207-266	Sequence 266, App	C 330	16	1.5	31	5	PCT-US94-02233-25	Sequence 25, Appl
C 258	16.4	1.5	50	4	US-09-262-142-49	Sequence 4648, Ap	C 331	16	1.5	33	2	US-08-841-178-11	Sequence 11, Appl
C 259	16.4	1.5	50	4	US-08-584-040-4648	Sequence 4648, Ap	C 332	16	1.5	34	4	US-08-315-241-23	Sequence 23, Appl
C 260	16.2	1.5	27	4	US-08-584-040-4648	Sequence 4648, Ap	C 333	16	1.5	35	5	PCT-US92-06611A-25	Sequence 25, Appl
C 261	16.2	1.5	30	2	US-08-629-001A-104	Sequence 7147, Ap	C 334	16	1.5	35	5	US-08-319-492B-236	Sequence 236, App
C 262	16.2	1.5	30	2	US-08-174-672D-43	Sequence 104, App	C 335	16	1.5	36	1	US-08-319-492B-236	Sequence 236, App
C 263	16.2	1.5	30	2	US-08-642-274D-183	Sequence 43, Appl	C 336	16	1.5	36	1	US-08-319-492B-236	Sequence 236, App
C 264	16.2	1.5	33	2	US-08-587-680A-21	Sequence 183, App	C 337	16	1.5	36	1	US-08-319-492B-236	Sequence 236, App
C 265	16.2	1.5	34	1	US-08-373-124A-31	Sequence 31, Appl	C 338	16	1.5	36	1	US-08-319-492B-236	Sequence 236, App
C 266	16.2	1.5	35	4	US-08-435-628-31	Sequence 31, Appl	C 339	16	1.5	37	1	US-08-323-084A-17	Sequence 17, Appl
C 267	16.2	1.5	35	4	US-08-973-005A-7	Sequence 7, Appl	C 340	16	1.5	37	1	US-08-255-670A-10	Sequence 10, Appl
C 268	16.2	1.5	36	1	US-08-468-557-5	Sequence 5, Appl	C 341	16	1.5	37	1	US-08-674-008-17	Sequence 17, Appl
C 269	16.2	1.5	36	2	US-08-585-684B-407	Sequence 407, App	C 342	16	1.5	37	6	RE34606-19	Sequence 17, Appl
C 270	16.2	1.5	36	2	US-09-038-073-407	Sequence 407, App	C 343	16	1.5	38	1	US-08-322-619-26	Sequence 26, Appl
C 271	16.2	1.5	38	4	US-09-262-173-103	Sequence 103, App	C 344	16	1.5	38	3	US-09-181-183-26	Sequence 26, Appl
C 272	16.2	1.5	40	1	US-08-086-428B-103	Sequence 103, App	C 345	16	1.5	38	4	US-09-277-700-26	Sequence 26, Appl
C 273	16.2	1.5	40	2	US-08-468-570-103	Sequence 103, App	C 346	16	1.5	38	5	PCT-US95-04075-26	Sequence 26, Appl
C 274	16.2	1.5	40	2	US-08-290-665A-207	Sequence 207, App	C 347	16	1.5	39	1	US-08-461-598-95	Sequence 95, Appl
C 275	16.2	1.5	40	5	PCT-US95-10398-207	Sequence 207, App	C 348	16	1.5	39	2	US-08-322-137-95	Sequence 95, Appl
C 276	16.2	1.5	41	3	US-08-836-504A-11	Sequence 11, Appl	C 349	16	1.5	39	4	US-08-582-333B-31	Sequence 31, Appl
C 277	16.2	1.5	41	4	US-08-804-166-20	Sequence 20, Appl	C 350	16	1.5	40	1	US-08-089-458B-3	Sequence 3, Appl
C 278	16.2	1.5	41	4	US-08-910-991-20	Sequence 20, Appl	C 351	16	1.5	40	4	US-09-056-998-48	Sequence 48, Appl
C 279	16.2	1.5	43	3	US-09-361-434-25	Sequence 25, Appl	C 352	16	1.5	40	4	US-09-052-521C-17	Sequence 17, Appl
C 280	16.2	1.5	44	1	US-07-686-591-1	Sequence 1, Appl	C 353	16	1.5	42	2	US-08-595-043A-63	Sequence 63, Appl
C 281	16.2	1.5	44	1	US-07-970-715-1	Sequence 7, Appl	C 354	16	1.5	42	2	US-08-244-548-9	Sequence 9, Appl
C 282	16.2	1.5	44	1	US-08-672-564-7	Sequence 383, App	C 355	16	1.5	42	3	US-08-879-565-8	Sequence 8, Appl
C 283	16.2	1.5	44	4	US-09-042-353-383	Sequence 233, App	C 356	16	1.5	42	3	US-08-438-562-17	Sequence 17, Appl
C 284	16.2	1.5	44	4	US-08-758-417A-233	Sequence 233, App	C 357	16	1.5	45	4	US-09-315-794-46	Sequence 46, Appl
C 285	16.2	1.5	44	6	5464756-29	Sequence 16, Appl	C 358	16	1.5	45	4	US-08-389-341-46	Sequence 46, Appl
C 286	16.2	1.5	45	4	US-09-091-814-16	Sequence 22, Appl	C 359	16	1.5	46	1	US-08-454-683-2	Sequence 2, Appl
C 287	16.2	1.5	46	2	US-08-452-724A-22	Sequence 22, Appl	C 360	16	1.5	46	1	US-08-454-683-2	Sequence 2, Appl
C 288	16.2	1.5	47	4	US-09-338-907-291	Sequence 291, App	C 361	16	1.5	46	2	US-08-116-778E-17	Sequence 17, Appl
C 289	16.2	1.5	47	4	US-09-218-207-291	Sequence 21, App	C 362	16	1.5	46	2	US-08-454-680-2	Sequence 2, Appl
C 290	16.2	1.5	47	6	5519127-1	Sequence 9, Appl	C 363	16	1.5	46	2	US-08-454-680-2	Sequence 2, Appl
C 291	16.2	1.5	48	1	US-07-797-556-9	Sequence 8, Appl	C 364	16	1.5	46	2	US-08-438-562-17	Sequence 17, Appl
C 292	16.2	1.5	48	3	US-09-205-428-8	Sequence 58, Appl	C 365	16	1.5	46	2	US-08-648-657-9	Sequence 7, Appl
C 293	16.2	1.5	49	4	US-09-091-814-58	Sequence 68, Appl	C 366	16	1.5	46	3	US-08-483-528B-17	Sequence 17, Appl
C 294	16.2	1.5	49	4	US-08-849-567A-68	Sequence 1679, Ap	C 367	16	1.5	47	1	US-08-673-799C-17	Sequence 17, Appl
C 295	16.2	1.5	50	1	US-08-171-389-214	Sequence 214, App	C 368	16	1.5	47	1	US-08-091-569-14	Sequence 14, Appl
C 296	16.2	1.5	50	1	US-08-445-640-19	Sequence 19, Appl	C 369	16	1.5	47	2	US-08-203-676-14	Sequence 14, Appl
C 297	16.2	1.5	50	1	US-08-123-936-214	Sequence 214, App	C 370	16	1.5	47	2	US-08-822-238-14	Sequence 14, Appl
C 298	16.2	1.5	50	3	US-08-985-162-1705	Sequence 1671, Ap	C 371	16	1.5	48	3	US-08-789-333E-76	Sequence 76, Appl
C 299	16.2	1.5	50	3	US-08-985-162-1705	Sequence 1671, Ap	C 372	16	1.5	48	3	US-08-789-333E-76	Sequence 76, Appl
C 300	16.2	1.5	50	3	US-08-482-080A-214	Sequence 214, App	C 373	16	1.5	48	4	US-09-167-375-26	Sequence 26, Appl
C 301	16.2	1.5	50	3	US-08-170-558-19	Sequence 19, Appl	C 374	16	1.5	50	1	US-08-171-389-214	Sequence 21, Appl
C 302	16.2	1.5	50	3	US-08-985-162-1679	Sequence 1671, Ap	C 375	16	1.5	50	1	US-08-367-175A-25	Sequence 25, Appl
C 303	16.2	1.5	50	3	US-08-985-162-1679	Sequence 1671, Ap	C 376	16	1.5	50	1	US-08-367-175A-25	Sequence 25, Appl
C 304	16.2	1.5	50	3	US-08-985-162-1705	Sequence 1705, Ap	C 377	16	1.5	50	1	US-08-442-513A-1	Sequence 1, Appl
C 305	16.2	1.5	50	3	US-08-447-314-19	Sequence 19, Appl	C 378	16	1.5	50	2	US-08-123-936-455	Sequence 455, App
C 306	16.2	1.5	50	3	US-08-445-461-19	Sequence 19, Appl	C 379	16	1.5	50	2	US-08-485-689-57	Sequence 57, Appl
C 307	16.2	1.5	50	4	US-09-339-913B-101	Sequence 101, App	C 380	16	1.5	50	2	US-08-485-689-57	Sequence 57, Appl
C 308	16.2	1.5	50	4	US-09-339-904A-101	Sequence 101, App	C 381	16	1.5	50	2	US-08-476-021A-60	Sequence 60, Appl
C 309	16.2	1.5	50	4	US-08-769-062B-101	Sequence 101, App	C 382	16	1.5	50	2	US-08-476-021A-60	Sequence 60, Appl
C 310	16.2	1.5	50	4	US-09-344-002B-101	Sequence 101, App	C 383	16	1.5	50	2	US-08-476-021A-60	Sequence 60, Appl
C 311	16.2	1.5	50	5	PCT-US93-12388-214	Sequence 214, App	C 384	16	1.5	50	2	US-08-476-021A-60	Sequence 60, Appl
C 312	16.2	1.5	25	2	US-08-466-103A-27	Sequence 27, Appl	C 385	16	1.5	50	3	US-08-478-608B-60	Sequence 60, Appl
C 313	16.2	1.5	25	2	US-08-466-103A-27	Sequence 27, Appl	C 386	16	1.5	50	3	US-08-482-080A-455	Sequence 455, App
C 314	16.2	1.5	25	3	US-08-486-382-6	Sequence 6, Appl	C 387	16	1.5	50	3	US-08-998-099-302	Sequence 302, App
C 315	16.2	1.5	25	3	US-09-235-546-6	Sequence 6, Appl	C 388	16	1.5	50	4	US-08-998-099-302	Sequence 302, App
C 316	16.2	1.5	26	2	US-08-859-998-956	Sequence 956, App	C 389	16	1.5	50	4	US-08-476-423A-60	Sequence 60, Appl
C 317	16.2	1.5	26	2	US-08-859-998-956	Sequence 956, App	C 390	16	1.5	50	4	PCT-US93-12388-455	Sequence 455, App
C 318	16.2	1.5	26	4	US-09-225-928-956	Sequence 956, App	C 391	16	1.5	27	3	US-08-513-974B-161	Sequence 161, App
C 319	16.2	1.5	27	4	US-09-225-928-956	Sequence 956, App	C 392	16	1.5	27	4	US-08-584-040-3201	Sequence 3201, Ap
					Sequence 466, App							PCT-US95-03866-21	Sequence 21, Appl

393	15.8	1.5	28	3	US-08-544-381B-96	Sequence 96, Appl	C 466	15.8	1.5	50	1	US-07-903-456-7	Sequence 7, Appl
394	15.8	1.5	28	4	US-09-162-021B-17	Sequence 17, Appl	C 467	15.8	1.5	50	1	US-07-903-456-8	Sequence 8, Appl
395	15.8	1.5	29	1	US-09-586-719-12	Sequence 12, Appl	C 468	15.8	1.5	50	1	US-08-471-206-26	Sequence 26, Appl
396	15.8	1.5	30	1	US-08-558-545-5	Sequence 5, Appl	C 469	15.8	1.5	50	1	US-08-281-025D-19	Sequence 19, Appl
397	15.8	1.5	30	1	US-08-456-103-2	Sequence 2, Appl	C 470	15.8	1.5	50	1	US-08-374-641-39	Sequence 39, Appl
398	15.8	1.5	30	2	US-09-067-908-2	Sequence 5, Appl	C 471	15.8	1.5	50	4	US-08-563-524A-14	Sequence 14, Appl
399	15.8	1.5	30	2	US-08-779-596A-5	Sequence 5, Appl	C 472	15.8	1.5	50	4	US-08-563-524A-15	Sequence 15, Appl
400	15.8	1.5	30	2	US-08-629-001A-64	Sequence 64, Appl	C 473	15.8	1.5	50	4	US-08-563-524A-17	Sequence 17, Appl
401	15.8	1.5	30	4	US-08-642-274D-143	Sequence 143, Appl	C 474	15.8	1.5	50	4	US-08-563-524A-18	Sequence 18, Appl
402	15.8	1.5	31	2	US-09-001-826-27	Sequence 27, Appl	C 475	15.8	1.5	50	4	US-09-227-717-6	Sequence 6, Appl
403	15.8	1.5	31	2	US-08-186-895-5	Sequence 5, Appl	C 476	15.6	1.4	22	2	US-08-486-382-5	Sequence 5, Appl
404	15.8	1.5	33	1	US-08-683-877-10	Sequence 10, Appl	C 477	15.6	1.4	22	3	US-09-235-546-5	Sequence 5, Appl
405	15.8	1.5	33	1	US-08-686-968C-47	Sequence 47, Appl	C 478	15.6	1.4	27	3	US-08-471-796-278	Sequence 278, Appl
406	15.8	1.5	34	3	US-08-836-561-12	Sequence 12, Appl	C 479	15.6	1.4	27	3	US-08-471-039-278	Sequence 1026, Appl
407	15.8	1.5	35	1	US-07-876-280-24	Sequence 24, Appl	C 480	15.6	1.4	27	3	US-08-584-040-1026	Sequence 6, Appl
408	15.8	1.5	35	1	US-07-935-310A-12	Sequence 12, Appl	C 481	15.6	1.4	27	5	PCT-US93-11198-278	Sequence 8, Appl
409	15.8	1.5	35	1	US-07-968-781A-26	Sequence 26, Appl	C 482	15.6	1.4	30	2	US-08-600-999-8	Sequence 2, Appl
410	15.8	1.5	35	1	US-08-147-189-12	Sequence 12, Appl	C 483	15.6	1.4	30	4	US-08-481-190-2	Sequence 2, Appl
411	15.8	1.5	35	1	US-07-991-867B-17	Sequence 17, Appl	C 484	15.6	1.4	30	5	US-08-229-515A-19	Sequence 19, Appl
412	15.8	1.5	35	1	US-08-107-755A-17	Sequence 17, Appl	C 485	15.6	1.4	31	1	US-08-645-865-19	Sequence 10, Appl
413	15.8	1.5	35	1	US-08-316-301A-38	Sequence 38, Appl	C 486	15.6	1.4	31	1	US-08-480-449-10	Sequence 10, Appl
414	15.8	1.5	35	2	US-08-544-332-17	Sequence 17, Appl	C 487	15.6	1.4	31	2	US-08-660-542-10	Sequence 13, Appl
415	15.8	1.5	35	2	US-09-076-137-38	Sequence 38, Appl	C 488	15.6	1.4	31	2	US-08-642-406A-13	Sequence 15, Appl
416	15.8	1.5	35	5	PCT-US92-03624-38	Sequence 38, Appl	C 489	15.6	1.4	31	3	US-08-434-000A-15	Sequence 15, Appl
417	15.8	1.5	35	5	PCT-US93-07409-12	Sequence 12, Appl	C 490	15.6	1.4	31	4	US-09-312-157-15	Sequence 10, Appl
418	15.8	1.5	36	1	US-08-363-240A-962	Sequence 962, Appl	C 491	15.6	1.4	31	4	US-08-479-603-10	Sequence 13, Appl
419	15.8	1.5	36	2	US-08-585-684B-963	Sequence 963, Appl	C 492	15.6	1.4	31	4	US-09-199-534-13	Sequence 16, Appl
420	15.8	1.5	36	4	US-09-038-073-963	Sequence 963, Appl	C 493	15.6	1.4	31	5	PCT-US93-08339-16	Sequence 22, Appl
421	15.8	1.5	36	4	US-09-041-878-4	Sequence 4, Appl	C 494	15.6	1.4	31	5	US-08-309-560-22	Sequence 11, Appl
422	15.8	1.5	38	1	US-08-373-124A-319	Sequence 319, Appl	C 495	15.6	1.4	32	1	US-08-125-012-11	Sequence 11, Appl
423	15.8	1.5	38	1	US-08-373-124A-1342	Sequence 1342, Appl	C 496	15.6	1.4	32	1	US-08-822-579A-1	Sequence 4, Appl
424	15.8	1.5	38	1	US-08-435-628-319	Sequence 319, Appl	C 497	15.6	1.4	32	1	US-08-221-579A-1	Sequence 1, Appl
425	15.8	1.5	38	4	US-08-435-628-1342	Sequence 1342, Appl	C 498	15.6	1.4	32	1	US-08-783-818-1	Sequence 11, Appl
426	15.8	1.5	38	4	US-09-316-083-33	Sequence 33, Appl	C 499	15.6	1.4	32	1	US-08-897-043-6	Sequence 6, Appl
427	15.8	1.5	38	5	PCT-US93-08329-10	Sequence 10, Appl	C 500	15.6	1.4	32	2	US-08-897-043-6	Sequence 1, Appl
428	15.8	1.5	39	4	US-09-262-773-117	Sequence 117, Appl	C 501	15.6	1.4	32	2	US-08-979-385B-1	Sequence 1, Appl
429	15.8	1.5	40	4	US-09-262-773-156	Sequence 156, Appl	C 502	15.6	1.4	32	2	US-08-979-385B-1	Sequence 1, Appl
430	15.8	1.5	40	6	US-08-390-874C-3	Sequence 3, Appl	C 503	15.6	1.4	32	2	US-08-979-385B-1	Sequence 1, Appl
431	15.8	1.5	41	3	US-08-813-507-41	Sequence 41, Appl	C 504	15.6	1.4	32	2	US-08-979-385B-1	Sequence 1, Appl
432	15.8	1.5	41	3	US-09-265-772-3	Sequence 3, Appl	C 505	15.6	1.4	32	2	US-08-979-385B-1	Sequence 1, Appl
433	15.8	1.5	41	4	US-09-464-453-41	Sequence 41, Appl	C 506	15.6	1.4	32	2	US-08-979-385B-1	Sequence 1, Appl
434	15.8	1.5	41	4	US-08-874-102-25	Sequence 25, Appl	C 507	15.6	1.4	32	2	US-08-979-385B-1	Sequence 1, Appl
435	15.8	1.5	42	4	US-09-387-300-24	Sequence 24, Appl	C 508	15.6	1.4	32	2	US-08-979-385B-1	Sequence 1, Appl
436	15.8	1.5	42	4	US-08-672-213-66	Sequence 66, Appl	C 509	15.6	1.4	32	2	US-08-979-385B-1	Sequence 1, Appl
437	15.8	1.5	43	4	US-08-672-213-66	Sequence 66, Appl	C 510	15.6	1.4	32	2	US-08-979-385B-1	Sequence 1, Appl
438	15.8	1.5	43	5	PCT-US95-17111A-8	Sequence 8, Appl	C 511	15.6	1.4	32	2	US-08-979-385B-1	Sequence 1, Appl
439	15.8	1.5	43	5	US-08-876-715-3	Sequence 3, Appl	C 512	15.6	1.4	32	2	US-08-979-385B-1	Sequence 1, Appl
440	15.8	1.5	45	4	US-09-537-357-46	Sequence 46, Appl	C 513	15.6	1.4	34	1	US-08-645-865-3	Sequence 3, Appl
441	15.8	1.5	45	5	PCT-US96-00888-13	Sequence 13, Appl	C 514	15.6	1.4	34	1	US-08-645-865-3	Sequence 3, Appl
442	15.8	1.5	46	1	US-08-096-762-207	Sequence 207, Appl	C 515	15.6	1.4	34	1	US-08-645-865-3	Sequence 3, Appl
443	15.8	1.5	46	2	US-08-596-387B-68	Sequence 68, Appl	C 516	15.6	1.4	34	1	US-08-645-865-3	Sequence 3, Appl
444	15.8	1.5	46	4	US-09-042-353-321	Sequence 321, Appl	C 517	15.6	1.4	34	2	US-08-645-865-3	Sequence 3, Appl
445	15.8	1.5	46	4	US-08-758-417A-169	Sequence 169, Appl	C 518	15.6	1.4	34	2	US-08-645-865-3	Sequence 3, Appl
446	15.8	1.5	46	4	US-09-067-615-68	Sequence 68, Appl	C 519	15.6	1.4	35	5	PCT-US96-08173-1	Sequence 23, Appl
447	15.8	1.5	47	1	PCT-US95-09816A-68	Sequence 68, Appl	C 520	15.6	1.4	36	1	US-07-794-440-13	Sequence 13, Appl
448	15.8	1.5	47	1	US-08-105-483-401	Sequence 401, Appl	C 521	15.6	1.4	36	1	US-08-041-648-13	Sequence 28, Appl
449	15.8	1.5	47	1	US-08-171-389-149	Sequence 149, Appl	C 522	15.6	1.4	36	1	US-08-397-470-23	Sequence 948, Appl
450	15.8	1.5	47	1	US-08-123-936-149	Sequence 149, Appl	C 523	15.6	1.4	36	3	US-08-645-865-28	Sequence 28, Appl
451	15.8	1.5	47	1	US-08-709-209-401	Sequence 401, Appl	C 524	15.6	1.4	36	3	US-08-645-865-28	Sequence 28, Appl
452	15.8	1.5	47	1	US-08-303-275-105	Sequence 105, Appl	C 525	15.6	1.4	36	3	US-08-645-865-28	Sequence 28, Appl
453	15.8	1.5	47	1	US-08-458-101-401	Sequence 401, Appl	C 526	15.6	1.4	36	4	US-09-214-151-2	Sequence 2, Appl
454	15.8	1.5	47	2	US-08-475-228A-149	Sequence 149, Appl	C 527	15.6	1.4	36	4	US-09-214-151-2	Sequence 2, Appl
455	15.8	1.5	47	3	US-08-482-080A-149	Sequence 149, Appl	C 528	15.6	1.4	36	4	US-09-214-151-2	Sequence 2, Appl
456	15.8	1.5	48	1	PCT-US93-12388-119	Sequence 119, Appl	C 529	15.6	1.4	36	4	US-09-214-151-2	Sequence 2, Appl
457	15.8	1.5	48	1	US-08-634-060-111	Sequence 111, Appl	C 530	15.6	1.4	37	2	US-08-337-315A-9	Sequence 9, Appl
458	15.8	1.5	48	1	US-08-709-515-11	Sequence 11, Appl	C 531	15.6	1.4	37	2	US-08-337-315A-9	Sequence 9, Appl
459	15.8	1.5	48	2	US-08-865-675-1	Sequence 1, Appl	C 532	15.6	1.4	38	1	US-08-390-850-766	Sequence 766, Appl
460	15.8	1.5	48	2	US-09-237-510-1	Sequence 10, Appl	C 533	15.6	1.4	38	1	US-08-390-850-766	Sequence 766, Appl
461	15.8	1.5	48	2	US-08-964-020-10	Sequence 58, Appl	C 534	15.6	1.4	38	1	US-08-435-634-766	Sequence 14, Appl
462	15.8	1.5	49	1	US-08-207-901-58	Sequence 24, Appl	C 535	15.6	1.4	38	1	US-08-435-634-766	Sequence 14, Appl
463	15.8	1.5	49	2	US-08-558-269-24	Sequence 24, Appl	C 536	15.6	1.4	38	1	US-08-435-634-766	Sequence 14, Appl
464	15.8	1.5	49	2	US-09-410-882-24	Sequence 24, Appl	C 537	15.6	1.4	38	1	US-08-435-634-766	Sequence 14, Appl
465	15.8	1.5	49	4	US-09-410-882-24	Sequence 24, Appl	C 538	15.6	1.4	38	2	US-08-537-811-11	Sequence 11, Appl

C 539	15.6	1.4	39	1	US-08-672-1588-15	Sequence 15, Appl	612	15.4	1.4	35	1	US-08-753-054-5	Sequence 5, Appl
C 540	15.6	1.4	39	1	US-08-231-342-11	Sequence 11, Appl	C 613	15.4	1.4	35	1	US-08-454-683-6	Sequence 6, Appl
C 541	15.6	1.4	39	3	US-08-875-223-6	Sequence 23, Appl	C 614	15.4	1.4	35	2	US-08-116-778E-21	Sequence 21, Appl
C 542	15.6	1.4	40	3	US-09-023-173-23	Sequence 23, Appl	C 615	15.4	1.4	35	2	US-08-454-680-6	Sequence 6, Appl
C 543	15.6	1.4	40	3	US-09-023-339-22	Sequence 22, Appl	C 616	15.4	1.4	35	2	US-08-438-562-21	Sequence 21, Appl
C 544	15.6	1.4	40	3	US-09-358-972-212	Sequence 212, Appl	C 617	15.4	1.4	35	2	US-08-959-638-5	Sequence 5, Appl
C 545	15.6	1.4	40	4	US-09-406-064-78	Sequence 78, Appl	C 618	15.4	1.4	35	2	US-08-483-528B-21	Sequence 21, Appl
C 546	15.6	1.4	40	4	US-09-430-615-48	Sequence 48, Appl	C 619	15.4	1.4	35	3	US-08-673-799C-21	Sequence 21, Appl
C 547	15.6	1.4	40	4	US-09-406-065-53	Sequence 53, Appl	C 620	15.4	1.4	35	3	US-08-328-673A-5	Sequence 5, Appl
C 548	15.6	1.4	42	6	5240838-8	Patent No. 5240838	C 621	15.4	1.4	36	1	US-08-363-240A-313	Sequence 313, Appl
C 549	15.6	1.4	45	3	US-08-931-220-44	Sequence 44, Appl	C 622	15.4	1.4	36	1	US-08-363-240A-310	Sequence 310, Appl
C 550	15.6	1.4	45	3	PCT-US95-11723-44	Sequence 44, Appl	C 623	15.4	1.4	36	1	US-08-363-240A-825	Sequence 825, Appl
C 551	15.6	1.4	45	5	PCT-US96-05997-44	Sequence 44, Appl	C 624	15.4	1.4	36	1	US-08-363-240A-826	Sequence 826, Appl
C 552	15.6	1.4	46	3	US-08-646-538-30	Sequence 30, Appl	C 625	15.4	1.4	36	1	US-08-363-240A-827	Sequence 827, Appl
C 553	15.6	1.4	46	4	US-09-503-222-30	Sequence 30, Appl	C 626	15.4	1.4	36	1	US-08-363-240A-828	Sequence 828, Appl
C 554	15.6	1.4	47	1	US-08-374-641-37	Sequence 37, Appl	C 627	15.4	1.4	36	1	US-08-311-486C-281	Sequence 281, Appl
C 555	15.6	1.4	47	1	US-08-231-342-21	Sequence 21, Appl	C 628	15.4	1.4	36	1	US-08-311-486C-354	Sequence 354, Appl
C 556	15.6	1.4	47	2	US-08-996-306-23	Sequence 23, Appl	C 629	15.4	1.4	36	1	US-08-311-486C-788	Sequence 788, Appl
C 557	15.6	1.4	47	4	US-09-338-907-23	Sequence 23, Appl	C 630	15.4	1.4	36	1	US-08-311-486C-879	Sequence 879, Appl
C 558	15.6	1.4	47	4	US-09-338-907-190	Sequence 190, Appl	C 631	15.4	1.4	36	2	US-08-585-684B-902	Sequence 902, Appl
C 559	15.6	1.4	47	4	US-09-218-207-251	Sequence 251, Appl	C 632	15.4	1.4	36	2	US-08-585-684B-903	Sequence 903, Appl
C 560	15.6	1.4	47	4	US-09-218-207-23	Sequence 23, Appl	C 633	15.4	1.4	36	2	US-08-585-684B-904	Sequence 904, Appl
C 561	15.6	1.4	47	4	US-09-218-207-190	Sequence 190, Appl	C 634	15.4	1.4	36	4	US-09-038-073-902	Sequence 902, Appl
C 562	15.6	1.4	47	4	US-09-218-207-251	Sequence 251, Appl	C 635	15.4	1.4	36	4	US-09-038-073-903	Sequence 903, Appl
C 563	15.6	1.4	48	2	US-08-804-794-3	Sequence 3, Appl	C 636	15.4	1.4	36	4	US-09-038-073-904	Sequence 904, Appl
C 564	15.6	1.4	48	4	US-09-299-450-3	Sequence 3, Appl	C 637	15.4	1.4	36	5	PCT-US93-05240-8	Sequence 2298
C 565	15.6	1.4	49	4	US-09-400-541-10	Sequence 10, Appl	C 638	15.4	1.4	37	4	US-09-332-478-21	Sequence 21, Appl
C 566	15.6	1.4	50	1	US-08-171-389-326	Sequence 326, Appl	C 639	15.4	1.4	37	4	US-09-332-477-15	Sequence 15, Appl
C 567	15.6	1.4	50	1	US-08-171-389-557	Sequence 557, Appl	C 640	15.4	1.4	38	1	US-08-328-314-11	Sequence 11, Appl
C 568	15.6	1.4	50	1	US-08-171-389-557	Sequence 557, Appl	C 641	15.4	1.4	38	1	US-08-731-045-11	Sequence 11, Appl
C 569	15.6	1.4	50	1	US-08-207-901-57	Sequence 78, Appl	C 642	15.4	1.4	38	2	US-08-731-045-11	Sequence 11, Appl
C 570	15.6	1.4	50	1	US-08-207-901-78	Sequence 78, Appl	C 643	15.4	1.4	38	2	US-08-292-620A-2298	Sequence 2298, Appl
C 571	15.6	1.4	50	1	US-08-123-936-326	Sequence 326, Appl	C 644	15.4	1.4	38	3	US-08-285-936-41	Sequence 41, Appl
C 572	15.6	1.4	50	2	US-08-475-228A-326	Sequence 326, Appl	C 645	15.4	1.4	39	1	US-08-887-86A-41	Sequence 41, Appl
C 573	15.6	1.4	50	2	US-08-475-228A-557	Sequence 557, Appl	C 646	15.4	1.4	39	2	US-08-860-1174A-21	Sequence 21, Appl
C 574	15.6	1.4	50	3	US-08-482-080A-326	Sequence 326, Appl	C 647	15.4	1.4	39	3	US-08-860-1174A-21	Sequence 21, Appl
C 575	15.6	1.4	50	3	US-08-482-080A-557	Sequence 557, Appl	C 648	15.4	1.4	39	3	US-08-860-1174A-21	Sequence 21, Appl
C 576	15.6	1.4	50	3	US-08-985-162-1656	Sequence 1656, Appl	C 649	15.4	1.4	40	2	US-08-771-025-11	Sequence 11, Appl
C 577	15.6	1.4	50	3	US-08-985-162-1690	Sequence 1690, Appl	C 650	15.4	1.4	40	2	US-08-249-189-7	Sequence 7, Appl
C 578	15.6	1.4	50	3	US-08-985-162-1716	Sequence 1716, Appl	C 651	15.4	1.4	40	2	US-08-484-624A-7	Sequence 7, Appl
C 579	15.6	1.4	50	3	US-08-985-162-1721	Sequence 1721, Appl	C 652	15.4	1.4	40	2	US-08-477-733B-7	Sequence 7, Appl
C 580	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 653	15.4	1.4	40	3	US-09-088-913A-7	Sequence 13, Appl
C 581	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 654	15.4	1.4	40	3	US-09-277-016-14	Sequence 14, Appl
C 582	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 655	15.4	1.4	40	4	US-09-416-050A-58	Sequence 58, Appl
C 583	15.6	1.4	50	3	US-08-985-162-1753	Sequence 1753, Appl	C 656	15.4	1.4	40	4	US-09-664-800-58	Sequence 58, Appl
C 584	15.6	1.4	50	5	PCT-US93-12388-326	Sequence 326, Appl	C 657	15.4	1.4	40	4	US-09-664-800-58	Sequence 58, Appl
C 585	15.6	1.4	50	5	PCT-US93-12388-326	Sequence 326, Appl	C 658	15.4	1.4	40	4	US-09-664-800-58	Sequence 58, Appl
C 586	15.4	1.4	25	1	US-08-316-293-19	Sequence 19, Appl	C 659	15.4	1.4	40	4	US-08-769-819-7	Sequence 7, Appl
C 587	15.4	1.4	25	1	US-08-488-702-2	Sequence 2, Appl	C 660	15.4	1.4	40	4	US-08-584-760A-57	Sequence 57, Appl
C 588	15.4	1.4	25	2	US-08-482-182-55	Sequence 55, Appl	C 661	15.4	1.4	40	4	US-08-770-974-7	Sequence 7, Appl
C 589	15.4	1.4	25	2	US-08-482-182-55	Sequence 55, Appl	C 662	15.4	1.4	41	3	US-08-721-458B-63	Sequence 63, Appl
C 590	15.4	1.4	27	1	US-08-381-280-21	Sequence 21, Appl	C 663	15.4	1.4	41	3	US-08-813-507-151	Sequence 151, Appl
C 591	15.4	1.4	27	2	US-08-445-533-21	Sequence 21, Appl	C 664	15.4	1.4	41	4	US-09-233-086-25	Sequence 25, Appl
C 592	15.4	1.4	27	3	US-08-985-162-1641	Sequence 1641, Appl	C 665	15.4	1.4	41	4	US-09-464-453-151	Sequence 151, Appl
C 593	15.4	1.4	27	3	US-09-052-085-21	Sequence 21, Appl	C 666	15.4	1.4	42	1	US-08-917-320-14	Sequence 14, Appl
C 594	15.4	1.4	27	4	US-09-012-097A-26	Sequence 26, Appl	C 667	15.4	1.4	42	2	US-08-917-320-14	Sequence 14, Appl
C 595	15.4	1.4	27	4	US-08-584-040-3545	Sequence 3545, Appl	C 668	15.4	1.4	42	2	US-08-942-521B-5	Sequence 5, Appl
C 596	15.4	1.4	27	4	US-08-584-040-4968	Sequence 4968, Appl	C 669	15.4	1.4	42	2	US-08-942-521B-5	Sequence 5, Appl
C 597	15.4	1.4	28	2	US-08-584-040-5158	Sequence 5158, Appl	C 670	15.4	1.4	42	3	US-08-783-774-16	Sequence 16, Appl
C 598	15.4	1.4	28	4	US-08-859-998-304	Sequence 304, Appl	C 671	15.4	1.4	42	4	US-09-192-702-5	Sequence 5, Appl
C 599	15.4	1.4	28	4	US-09-325-928-304	Sequence 304, Appl	C 672	15.4	1.4	42	4	US-09-396-281-9	Sequence 9, Appl
C 600	15.4	1.4	29	1	US-08-290-592E-13	Sequence 13, Appl	C 673	15.4	1.4	42	5	US-08-445-474-5	Sequence 5, Appl
C 601	15.4	1.4	29	5	PCT-US95-10053-10	Sequence 10, Appl	C 674	15.4	1.4	42	5	PCT-US94-02612-5	Sequence 5, Appl
C 602	15.4	1.4	29	5	PCT-US95-10053-10	Sequence 10, Appl	C 675	15.4	1.4	42	5	PCT-US95-04611A-14	Sequence 14, Appl
C 603	15.4	1.4	30	4	US-08-974-549A-548	Sequence 548, Appl	C 676	15.4	1.4	43	1	US-07-741-940-29	Sequence 29, Appl
C 604	15.4	1.4	30	4	US-08-696-932A-39	Sequence 39, Appl	C 677	15.4	1.4	43	1	US-08-289-548A-29	Sequence 29, Appl
C 605	15.4	1.4	31	1	US-08-390-850-189	Sequence 189, Appl	C 678	15.4	1.4	43	1	US-08-452-654-29	Sequence 29, Appl
C 606	15.4	1.4	31	1	US-08-435-634-189	Sequence 189, Appl	C 679	15.4	1.4	43	3	US-08-452-654-29	Sequence 29, Appl
C 607	15.4	1.4	32	2	US-08-859-998-429	Sequence 429, Appl	C 680	15.4	1.4	43	3	US-08-874-825-47	Sequence 47, Appl
C 608	15.4	1.4	32	4	US-09-225-928-429	Sequence 429, Appl	C 681	15.4	1.4	43	3	US-08-663-824-47	Sequence 47, Appl
C 609	15.4	1.4	33	2	US-08-483-636-56	Sequence 56, Appl	C 682	15.4	1.4	43	3	US-08-450-362-19	Sequence 19, Appl
C 610	15.4	1.4	33	2	US-08-483-632-56	Sequence 56, Appl	C 683	15.4	1.4	44	2	US-09-116-032-17	Sequence 17, Appl
C 611	15.4	1.4	35	1	US-08-408-133-6	Sequence 6, Appl	C 684	15.4	1.4	44	2	US-08-749-852-4	Sequence 4, Appl

C 685	15.4	1.4	44	4	US-09-042-353-372	Sequence 372, App	758	15.4	1.4	50	3	US-08-998-099-291	Sequence 291, App
C 686	15.4	1.4	44	4	US-08-758-417A-222	Sequence 222, App	759	15.4	1.4	50	3	US-08-998-099-295	Sequence 295, App
C 687	15.4	1.4	44	4	US-08-532-657A-4	Sequence 4, App11	760	15.4	1.4	50	3	US-08-998-099-296	Sequence 296, App
C 688	15.4	1.4	45	4	US-07-885-689A-5	Sequence 5, App11	761	15.4	1.4	50	3	US-08-998-099-299	Sequence 299, App
C 689	15.4	1.4	45	4	US-09-537-357-46	Sequence 46, App1	762	15.4	1.4	50	3	US-08-998-099-305	Sequence 305, App
C 690	15.4	1.4	45	4	US-09-423-439-49	Sequence 49, App1	763	15.4	1.4	50	3	US-08-998-099-308	Sequence 308, App
C 691	15.4	1.4	46	1	US-08-758-626-24	Sequence 24, App1	764	15.4	1.4	50	3	US-08-998-099-310	Sequence 310, App
C 692	15.4	1.4	46	2	US-08-615-961-11	Sequence 11, App1	765	15.4	1.4	50	3	US-08-998-099-312	Sequence 312, App
C 693	15.4	1.4	46	2	US-08-299-074A-7	Sequence 7, App11	766	15.4	1.4	50	3	US-08-998-099-316	Sequence 316, App
C 694	15.4	1.4	46	4	US-09-399-773-7	Sequence 24, App1	767	15.4	1.4	50	3	US-08-998-099-318	Sequence 318, App
C 695	15.4	1.4	46	5	PCT-US94-07684-24	Sequence 104, App	768	15.4	1.4	50	3	US-08-998-099-320	Sequence 320, App
C 696	15.4	1.4	47	1	US-08-171-389-104	Sequence 104, App	769	15.4	1.4	50	3	US-08-998-099-324	Sequence 324, App
C 697	15.4	1.4	47	1	US-08-123-936-104	Sequence 104, App	770	15.4	1.4	50	4	US-08-476-423A-12	Sequence 12, App1
C 698	15.4	1.4	47	2	US-08-350-161-8	Sequence 8, App11	771	15.4	1.4	50	4	US-08-476-423A-65	Sequence 65, App1
C 699	15.4	1.4	47	2	US-08-440-401-8	Sequence 8, App11	772	15.2	1.4	20	4	US-08-639-763-7	Sequence 48, App1
C 700	15.4	1.4	47	2	US-08-419-878B-8	Sequence 8, App11	773	15.2	1.4	20	4	US-09-487-445-56	Sequence 56, App1
C 701	15.4	1.4	47	2	US-08-475-228A-104	Sequence 104, App	774	15.2	1.4	20	4	US-09-662-249A-48	Sequence 7, App11
C 702	15.4	1.4	47	3	US-08-482-080A-104	Sequence 104, App	775	15.2	1.4	21	1	US-07-717-331F-7	Sequence 76, App1
C 703	15.4	1.4	47	5	PCT-US93-12388-104	Sequence 104, App	776	15.2	1.4	21	3	US-08-835-728D-76	Sequence 180, App
C 704	15.4	1.4	49	1	US-07-753-110B-10	Sequence 10, App1	777	15.2	1.4	21	3	US-08-835-728D-180	Sequence 180, App
C 705	15.4	1.4	49	1	US-08-086-634-10	Sequence 10, App1	778	15.2	1.4	21	4	US-09-490-558-76	Sequence 180, App
C 706	15.4	1.4	49	1	US-08-207-901-59	Sequence 59, App1	779	15.2	1.4	21	4	US-08-851-135-8	Sequence 85, App1
C 707	15.4	1.4	49	1	US-08-503-730-4	Sequence 4, App11	780	15.2	1.4	22	2	US-08-859-998-85	Sequence 85, App1
C 708	15.4	1.4	49	2	US-08-507-634-11	Sequence 11, App1	781	15.2	1.4	22	2	US-09-225-928-85	Sequence 85, App1
C 709	15.4	1.4	49	6	5221624-11	Patent No. 5221624	782	15.2	1.4	22	4	US-09-323-873A-5	Sequence 29, App1
C 710	15.4	1.4	50	1	US-07-828-44A-8	Sequence 12, App1	783	15.2	1.4	24	4	US-09-323-873A-29	Sequence 29, App1
C 711	15.4	1.4	50	2	US-08-485-689-12	Sequence 12, App1	784	15.2	1.4	24	4	US-08-375-116A-104	Sequence 29, App1
C 712	15.4	1.4	50	2	US-08-485-689-65	Sequence 65, App1	785	15.2	1.4	25	1	US-09-335-409-29	Sequence 29, App1
C 713	15.4	1.4	50	2	US-08-476-021A-65	Sequence 65, App1	786	15.2	1.4	25	4	US-09-567-962-29	Sequence 29, App1
C 714	15.4	1.4	50	2	US-08-476-021A-12	Sequence 12, App1	787	15.2	1.4	25	4	US-09-567-962-29	Sequence 29, App1
C 715	15.4	1.4	50	2	US-08-478-608B-12	Sequence 12, App1	788	15.2	1.4	25	4	US-09-568-480-29	Sequence 29, App1
C 716	15.4	1.4	50	2	US-08-478-608B-65	Sequence 65, App1	789	15.2	1.4	25	4	US-09-568-480-29	Sequence 29, App1
C 717	15.4	1.4	50	3	US-08-985-162-1647	Sequence 1647, App	790	15.2	1.4	25	4	US-09-568-480-29	Sequence 29, App1
C 718	15.4	1.4	50	3	US-08-985-162-1648	Sequence 1648, App	791	15.2	1.4	25	4	US-09-568-480-29	Sequence 29, App1
C 719	15.4	1.4	50	3	US-08-985-162-1651	Sequence 1651, App	792	15.2	1.4	26	2	US-09-568-480-29	Sequence 29, App1
C 720	15.4	1.4	50	3	US-08-985-162-1653	Sequence 1653, App	793	15.2	1.4	26	2	US-09-568-480-29	Sequence 29, App1
C 721	15.4	1.4	50	3	US-08-985-162-1658	Sequence 1658, App	794	15.2	1.4	26	2	US-09-568-480-29	Sequence 29, App1
C 722	15.4	1.4	50	3	US-08-985-162-1660	Sequence 1660, App	795	15.2	1.4	27	4	US-08-584-040-988	Sequence 988, App
C 723	15.4	1.4	50	3	US-08-985-162-1661	Sequence 1661, App	796	15.2	1.4	27	4	US-08-584-040-1013	Sequence 1013, App
C 724	15.4	1.4	50	3	US-08-985-162-1664	Sequence 1664, App	797	15.2	1.4	28	6	US-08-647-584-34	Sequence 34, App1
C 725	15.4	1.4	50	3	US-08-985-162-1668	Sequence 1668, App	798	15.2	1.4	28	6	5240838-7	Patent No. 5240838
C 726	15.4	1.4	50	3	US-08-985-162-1672	Sequence 1672, App	799	15.2	1.4	29	2	US-08-199-722-6	Sequence 6, App1
C 727	15.4	1.4	50	3	US-08-985-162-1673	Sequence 1673, App	800	15.2	1.4	29	4	US-09-358-972-236	Sequence 236, App
C 728	15.4	1.4	50	3	US-08-985-162-1676	Sequence 1676, App	801	15.2	1.4	29	4	US-09-430-615-26	Sequence 26, App1
C 729	15.4	1.4	50	3	US-08-985-162-1680	Sequence 1680, App	802	15.2	1.4	30	1	US-08-162-836-2	Sequence 2, App1
C 730	15.4	1.4	50	3	US-08-985-162-1687	Sequence 1687, App	803	15.2	1.4	30	3	US-08-445-463B-117	Sequence 117, App
C 731	15.4	1.4	50	3	US-08-985-162-1688	Sequence 1688, App	804	15.2	1.4	30	3	US-08-445-463B-117	Sequence 117, App
C 732	15.4	1.4	50	3	US-08-985-162-1689	Sequence 1689, App	805	15.2	1.4	30	3	US-08-445-463B-117	Sequence 117, App
C 733	15.4	1.4	50	3	US-08-985-162-1691	Sequence 1691, App	806	15.2	1.4	30	3	US-09-242-797-4	Sequence 4, App1
C 734	15.4	1.4	50	3	US-08-985-162-1692	Sequence 1692, App	807	15.2	1.4	30	3	US-08-445-464C-116	Sequence 116, App
C 735	15.4	1.4	50	3	US-08-985-162-1694	Sequence 1694, App	808	15.2	1.4	30	3	US-08-445-464C-117	Sequence 23, App1
C 736	15.4	1.4	50	3	US-08-985-162-1699	Sequence 1699, App	809	15.2	1.4	30	3	US-08-109-037-58	Sequence 58, App1
C 737	15.4	1.4	50	3	US-08-985-162-1700	Sequence 1700, App	810	15.2	1.4	30	3	US-08-109-037-58	Sequence 58, App1
C 738	15.4	1.4	50	3	US-08-985-162-1701	Sequence 1701, App	811	15.2	1.4	30	5	US-08-109-037-58	Sequence 58, App1
C 739	15.4	1.4	50	3	US-08-985-162-1702	Sequence 1702, App	812	15.2	1.4	30	5	US-08-109-037-58	Sequence 58, App1
C 740	15.4	1.4	50	3	US-08-985-162-1704	Sequence 1704, App	813	15.2	1.4	30	5	US-08-109-037-58	Sequence 58, App1
C 741	15.4	1.4	50	3	US-08-985-162-1707	Sequence 1707, App	814	15.2	1.4	31	1	PCT-US94-03437-117	Sequence 117, App
C 742	15.4	1.4	50	3	US-08-985-162-1709	Sequence 1709, App	815	15.2	1.4	31	1	US-08-276-852-39	Sequence 39, App1
C 743	15.4	1.4	50	3	US-08-985-162-1711	Sequence 1711, App	816	15.2	1.4	31	1	US-08-133-011-125	Sequence 125, App
C 744	15.4	1.4	50	3	US-08-985-162-1712	Sequence 1712, App	817	15.2	1.4	31	1	US-08-387-874-83	Sequence 83, App1
C 745	15.4	1.4	50	3	US-08-985-162-1713	Sequence 1713, App	818	15.2	1.4	31	1	US-08-899-575-39	Sequence 39, App1
C 746	15.4	1.4	50	3	US-08-985-162-1718	Sequence 1718, App	819	15.2	1.4	31	4	US-08-899-575-39	Sequence 39, App1
C 747	15.4	1.4	50	3	US-08-985-162-1723	Sequence 1723, App	820	15.2	1.4	31	4	US-08-899-575-39	Sequence 39, App1
C 748	15.4	1.4	50	3	US-08-985-162-1727	Sequence 1727, App	821	15.2	1.4	31	5	US-08-686-968C-86	Sequence 86, App1
C 749	15.4	1.4	50	3	US-08-985-162-1742	Sequence 1742, App	822	15.2	1.4	31	5	US-08-907-739-125	Sequence 125, App
C 750	15.4	1.4	50	3	US-08-985-162-1743	Sequence 1743, App	823	15.2	1.4	31	5	PCT-US93-08364-83	Sequence 83, App1
C 751	15.4	1.4	50	3	US-08-985-162-1752	Sequence 1752, App	824	15.2	1.4	31	5	PCT-US93-08364-83	Sequence 83, App1
C 752	15.4	1.4	50	3	US-08-985-162-1755	Sequence 1755, App	825	15.2	1.4	31	5	PCT-US93-08364-83	Sequence 83, App1
C 753	15.4	1.4	50	3	US-08-985-162-1757	Sequence 1757, App	826	15.2	1.4	32	1	PCT-US95-08743-39	Sequence 39, App1
C 754	15.4	1.4	50	3	US-08-998-099-281	Sequence 281, App	827	15.2	1.4	32	1	PCT-US95-13975-6	Sequence 24, App1
C 755	15.4	1.4	50	3	US-08-998-099-284	Sequence 284, App	828	15.2	1.4	32	1	US-08-095-043-21	Sequence 21, App1
C 756	15.4	1.4	50	3	US-08-998-099-285	Sequence 285, App	829	15.2	1.4	32	1	US-08-095-043-21	Sequence 21, App1
C 757	15.4	1.4	50	3	US-08-998-099-288	Sequence 288, App	830	15.2	1.4	33	1	US-08-093-577-17	Sequence 17, App1
												US-08-096-623A-29	Sequence 29, App1
												US-08-417-330A-7	Sequence 7, App11
												US-08-403-634-8	Sequence 8, App11



831	15.2	1.4	33	4	US-08-913-441B-8	Sequence 8, Appl1	904	15.2	1.4	39	2	US-08-491-334A-43	Sequence 43, Appl1
832	15.2	1.4	33	4	US-08-427-569-13	Sequence 13, Appl1	905	15.2	1.4	39	2	US-08-800-353-61	Sequence 61, Appl1
C 833	15.2	1.4	34	1	US-08-475-867A-10	Sequence 10, Appl1	C 906	15.2	1.4	39	2	US-08-800-353-62	Sequence 62, Appl1
C 834	15.2	1.4	34	1	US-08-477-883A-10	Sequence 10, Appl1	C 907	15.2	1.4	39	2	US-08-308-865-109	Sequence 109, Appl1
C 835	15.2	1.4	34	1	US-08-472-427A-10	Sequence 10, Appl1	C 908	15.2	1.4	39	2	US-08-308-865-110	Sequence 110, Appl1
C 836	15.2	1.4	34	1	US-08-315-287A-10	Sequence 10, Appl1	C 909	15.2	1.4	39	2	US-08-576-626A-6	Sequence 6, Appl1
C 837	15.2	1.4	34	4	US-09-091-305-4	Sequence 4, Appl1	C 910	15.2	1.4	39	3	US-09-027-449-11	Sequence 11, Appl1
C 838	15.2	1.4	35	1	US-07-931-473B-186	Sequence 186, App	C 911	15.2	1.4	39	3	US-08-804-444A-11	Sequence 11, Appl1
C 839	15.2	1.4	35	1	US-07-714-131C-186	Sequence 186, App	C 912	15.2	1.4	39	3	US-09-026-985-11	Sequence 11, Appl1
C 840	15.2	1.4	35	1	US-08-412-110-186	Sequence 186, App	C 913	15.2	1.4	39	3	US-09-277-016-15	Sequence 15, Appl1
C 841	15.2	1.4	35	1	US-08-403-442A-186	Sequence 186, App	C 914	15.2	1.4	39	4	US-09-042-353-302	Sequence 302, App
C 842	15.2	1.4	35	1	US-08-249-671A-3	Sequence 3, Appl1	C 915	15.2	1.4	39	4	US-08-758-417A-130	Sequence 303, App
C 843	15.2	1.4	35	2	US-08-469-609A-186	Sequence 186, App	C 916	15.2	1.4	39	4	US-08-758-417A-131	Sequence 151, App
C 844	15.2	1.4	35	3	US-09-143-190-186	Sequence 186, App	C 917	15.2	1.4	39	4	US-08-758-417A-131	Sequence 62, Appl1
C 845	15.2	1.4	35	4	US-09-581-617-10	Sequence 10, Appl1	C 918	15.2	1.4	39	4	US-08-758-417A-131	Sequence 109, App
C 846	15.2	1.4	36	1	US-08-477-270-2	Sequence 2, Appl1	C 919	15.2	1.4	39	5	PCT-US92-06185-61	Sequence 110, App
C 847	15.2	1.4	36	1	US-08-334-847-437	Sequence 437, App	C 920	15.2	1.4	39	5	PCT-US92-06185-62	Sequence 62, Appl1
C 848	15.2	1.4	36	1	US-08-334-847-689	Sequence 689, App	C 921	15.2	1.4	39	5	PCT-US92-10983-109	Sequence 109, App
C 849	15.2	1.4	36	1	US-07-936-421-15	Sequence 15, Appl1	C 922	15.2	1.4	39	5	PCT-US92-10983-110	Sequence 110, App
C 850	15.2	1.4	36	1	US-08-399-696-8	Sequence 8, Appl1	C 923	15.2	1.4	39	5	PCT-US85-10053-6	Sequence 6, Appl1
C 851	15.2	1.4	36	2	US-08-292-620A-793	Sequence 793, App	C 924	15.2	1.4	40	1	US-08-719-331-4	Sequence 4, Appl1
C 852	15.2	1.4	36	2	US-08-474-379C-75	Sequence 75, Appl1	C 925	15.2	1.4	40	2	US-08-767-979-8	Sequence 8, Appl1
C 853	15.2	1.4	36	3	US-09-146-249A-75	Sequence 75, Appl1	C 926	15.2	1.4	40	2	US-08-875-377-5	Sequence 8, Appl1
C 854	15.2	1.4	36	3	US-08-206-188B-75	Sequence 75, Appl1	C 927	15.2	1.4	40	4	US-09-295-026-8	Sequence 8, Appl1
C 855	15.2	1.4	36	3	US-09-071-845-793	Sequence 793, App	C 928	15.2	1.4	40	4	US-09-485-737B-8	Sequence 8, Appl1
C 856	15.2	1.4	36	4	US-09-101-126-11	Sequence 11, Appl1	C 929	15.2	1.4	41	1	US-08-328-152B-15	Sequence 15, Appl1
C 857	15.2	1.4	36	4	US-09-101-126-12	Sequence 12, Appl1	C 930	15.2	1.4	41	1	US-08-328-152B-15	Sequence 19, Appl1
C 858	15.2	1.4	37	3	US-09-066-597-22	Sequence 22, Appl1	C 931	15.2	1.4	41	2	US-08-783-853A-101	Sequence 101, App
C 859	15.2	1.4	38	1	US-08-373-124A-1572	Sequence 1572, App	C 932	15.2	1.4	42	1	US-08-160-670A-29	Sequence 29, App
C 860	15.2	1.4	38	1	US-08-373-124A-1974	Sequence 1974, App	C 933	15.2	1.4	42	1	US-08-375-116A-2	Sequence 2, Appl1
C 861	15.2	1.4	38	1	US-08-373-124A-2360	Sequence 2360, App	C 934	15.2	1.4	42	1	US-08-391-000-22	Sequence 22, Appl1
C 862	15.2	1.4	38	1	US-08-373-124A-2576	Sequence 2576, App	C 935	15.2	1.4	42	1	US-08-391-000-22	Sequence 22, Appl1
C 863	15.2	1.4	38	1	US-08-435-628-1572	Sequence 1572, App	C 936	15.2	1.4	42	2	US-08-679-645-14	Sequence 14, Appl1
C 864	15.2	1.4	38	1	US-08-435-628-1974	Sequence 1974, App	C 937	15.2	1.4	42	2	US-08-679-645-14	Sequence 14, Appl1
C 865	15.2	1.4	38	1	US-08-435-628-2360	Sequence 2360, App	C 938	15.2	1.4	43	2	US-08-857-946-116	Sequence 16, Appl1
C 866	15.2	1.4	38	1	US-08-435-628-2576	Sequence 2576, App	C 939	15.2	1.4	43	2	US-08-857-946-116	Sequence 16, Appl1
C 867	15.2	1.4	38	2	US-08-746-667-3	Sequence 6, Appl1	C 940	15.2	1.4	43	3	US-08-870-740-116	Sequence 116, App
C 868	15.2	1.4	38	2	US-09-120-577-6	Sequence 6, Appl1	C 941	15.2	1.4	43	3	US-08-832-985-70	Sequence 70, App
C 869	15.2	1.4	38	4	US-09-312-731-3	Sequence 3, Appl1	C 942	15.2	1.4	44	1	US-07-603-451A-8	Sequence 8, Appl1
C 870	15.2	1.4	38	4	US-09-338-913B-2	Sequence 2, Appl1	C 943	15.2	1.4	44	1	US-08-060-822A-9	Sequence 9, Appl1
C 871	15.2	1.4	38	4	US-09-338-913B-2	Sequence 2, Appl1	C 944	15.2	1.4	44	1	US-08-345-505A-9	Sequence 9, Appl1
C 872	15.2	1.4	38	4	US-08-769-062B-2	Sequence 2, Appl1	C 945	15.2	1.4	44	1	US-08-350-260A-181	Sequence 181, App
C 873	15.2	1.4	38	4	US-09-344-002B-2	Sequence 2, Appl1	C 946	15.2	1.4	44	5	PCT-US94-05257-9	Sequence 9, Appl1
C 874	15.2	1.4	38	5	PCT-US91-02568-15	Sequence 15, Appl1	C 947	15.2	1.4	45	1	US-08-067-684-12	Sequence 12, Appl1
C 875	15.2	1.4	38	5	PCT-US93-08329-9	Sequence 9, Appl1	C 948	15.2	1.4	45	1	US-08-171-389-107	Sequence 107, App
C 876	15.2	1.4	38	5	PCT-US95-06987-5	Sequence 5, Appl1	C 949	15.2	1.4	45	1	US-08-349-696-6	Sequence 6, Appl1
C 877	15.2	1.4	39	1	US-07-834-539A-61	Sequence 61, Appl1	C 950	15.2	1.4	45	1	US-08-560-231-6	Sequence 6, Appl1
C 878	15.2	1.4	39	1	US-07-834-539A-62	Sequence 62, Appl1	C 951	15.2	1.4	45	1	US-08-560-231-6	Sequence 6, Appl1
C 879	15.2	1.4	39	1	US-08-053-131-109	Sequence 109, App	C 952	15.2	1.4	45	1	US-08-582-257-17	Sequence 17, App
C 880	15.2	1.4	39	1	US-08-053-131-110	Sequence 110, App	C 953	15.2	1.4	45	1	US-08-582-257-17	Sequence 17, App
C 881	15.2	1.4	39	1	US-08-398-612A-11	Sequence 11, Appl1	C 954	15.2	1.4	45	1	US-08-447-169A-228	Sequence 228, App
C 882	15.2	1.4	39	1	US-08-398-612A-15	Sequence 15, Appl1	C 955	15.2	1.4	45	1	US-08-447-169A-228	Sequence 228, App
C 883	15.2	1.4	39	1	US-08-398-612A-43	Sequence 43, Appl1	C 956	15.2	1.4	45	2	US-08-447-169A-228	Sequence 12, Appl1
C 884	15.2	1.4	39	1	US-08-398-612A-11	Sequence 11, Appl1	C 957	15.2	1.4	45	2	US-08-447-169A-228	Sequence 12, Appl1
C 885	15.2	1.4	39	1	US-08-398-612A-15	Sequence 15, Appl1	C 958	15.2	1.4	45	2	US-08-447-169A-228	Sequence 12, Appl1
C 886	15.2	1.4	39	1	US-08-398-612A-43	Sequence 43, Appl1	C 959	15.2	1.4	45	2	US-08-447-169A-228	Sequence 12, Appl1
C 887	15.2	1.4	39	1	US-08-398-612A-11	Sequence 11, Appl1	C 960	15.2	1.4	45	2	US-08-447-169A-228	Sequence 12, Appl1
C 888	15.2	1.4	39	1	US-08-398-612A-15	Sequence 15, Appl1	C 961	15.2	1.4	45	2	US-08-447-169A-228	Sequence 12, Appl1
C 889	15.2	1.4	39	1	US-08-398-612A-43	Sequence 43, Appl1	C 962	15.2	1.4	45	2	US-08-447-169A-228	Sequence 12, Appl1
C 890	15.2	1.4	39	1	US-08-398-612A-11	Sequence 11, Appl1	C 963	15.2	1.4	45	2	US-08-447-169A-228	Sequence 12, Appl1
C 891	15.2	1.4	39	1	US-08-398-612A-15	Sequence 15, Appl1	C 964	15.2	1.4	45	2	US-08-447-169A-228	Sequence 12, Appl1
C 892	15.2	1.4	39	1	US-08-398-612A-43	Sequence 43, Appl1	C 965	15.2	1.4	45	2	US-08-447-169A-228	Sequence 12, Appl1
C 893	15.2	1.4	39	1	US-08-398-612A-11	Sequence 11, Appl1	C 966	15.2	1.4	45	2	US-08-447-169A-228	Sequence 12, Appl1
C 894	15.2	1.4	39	1	US-08-398-612A-15	Sequence 15, Appl1	C 967	15.2	1.4	45	2	US-08-447-169A-228	Sequence 12, Appl1
C 895	15.2	1.4	39	1	US-08-398-612A-43	Sequence 43, Appl1	C 968	15.2	1.4	45	2	US-08-447-169A-228	Sequence 12, Appl1
C 896	15.2	1.4	39	1	US-08-398-612A-11	Sequence 11, Appl1	C 969	15.2	1.4	45	2	US-08-447-169A-228	Sequence 12, Appl1
C 897	15.2	1.4	39	1	US-08-398-612A-15	Sequence 15, Appl1	C 970	15.2	1.4	45	2	US-08-447-169A-228	Sequence 12, Appl1
C 898	15.2	1.4	39	1	US-08-398-612A-43	Sequence 43, Appl1	C 971	15.2	1.4	45	2	US-08-447-169A-228	Sequence 12, Appl1
C 899	15.2	1.4	39	1	US-08-398-612A-11	Sequence 11, Appl1	C 972	15.2	1.4	45	2	US-08-447-169A-228	Sequence 12, Appl1
C 900	15.2	1.4	39	1	US-08-398-612A-15	Sequence 15, Appl1	C 973	15.2	1.4	45	2	US-08-447-169A-228	Sequence 12, Appl1
C 901	15.2	1.4	39	1	US-08-398-612A-43	Sequence 43, Appl1	C 974	15.2	1.4	45	2	US-08-447-169A-228	Sequence 12, Appl1
C 902	15.2	1.4	39	1	US-08-398-612A-11	Sequence 11, Appl1	C 975	15.2	1.4	45	2	US-08-447-169A-228	Sequence 12, Appl1
C 903	15.2	1.4	39	2	US-08-491-334A-11	Sequence 11, Appl1	C 976	15.2	1.4	46	3	PCT-US93-11198-40	Sequence 40, Appl1

c 977 15.2 1.4 46 5 PCT-US95-13975-35  
978 15.2 1.4 47 1 US-08-053-131-55  
979 15.2 1.4 47 1 US-08-645-641-55  
980 15.2 1.4 47 1 US-07-853-408B-55  
981 15.2 1.4 47 1 US-08-096-762-55  
982 15.2 1.4 47 2 US-08-308-865-55  
983 15.2 1.4 47 4 US-09-042-353-218  
984 15.2 1.4 47 4 US-09-338-907-260  
985 15.2 1.4 47 4 US-09-338-907-337  
986 15.2 1.4 47 4 US-08-758-417A-66  
987 15.2 1.4 47 4 US-08-849-567A-85  
988 15.2 1.4 47 4 US-09-218-207-260  
989 15.2 1.4 47 4 US-09-218-207-337  
990 15.2 1.4 47 5 PCT-US92-10983-55  
991 15.2 1.4 48 1 US-08-475-063-40  
992 15.2 1.4 48 1 US-08-207-792-40  
993 15.2 1.4 48 1 US-08-582-257-24  
994 15.2 1.4 48 2 US-08-582-298-24  
995 15.2 1.4 48 3 US-08-369-822C-37  
996 15.2 1.4 48 3 US-08-582-776C-52  
997 15.2 1.4 48 3 US-08-434-831B-49  
998 15.2 1.4 49 1 US-08-171-389-162  
999 15.2 1.4 49 1 US-08-123-936-162  
c1000 15.2 1.4 49 2 US-08-475-228A-162

## ALIGNMENTS

Sequence 35, Appl  
Sequence 55, Appl  
Sequence 55, Appl  
Sequence 55, Appl  
Sequence 55, Appl  
Sequence 55, Appl  
Sequence 218, App  
Sequence 260, App  
Sequence 337, App  
Sequence 66, Appl  
Sequence 85, Appl  
Sequence 260, App  
Sequence 337, App  
Sequence 55, Appl  
Sequence 40, Appl  
Sequence 24, Appl  
Sequence 24, Appl  
Sequence 37, Appl  
Sequence 52, Appl  
Sequence 48, Appl  
Sequence 162, App  
Sequence 162, App  
Sequence 162, App

RESULT 1  
US-08-660-626-13  
; Sequence 13, Application US/08660626  
; Patent No. 5789655  
; GENERAL INFORMATION:  
; APPLICANT: Stanley B. Prusiner  
; APPLICANT: Glenn C. Telling  
; APPLICANT: Fred E. Cohen  
; APPLICANT: Michael R. Scott  
; TITLE OF INVENTION: TRANSGENIC ANIMALS EXPRESSING  
; TITLE OF INVENTION: EPIPOPE-TAGGED PROTEINS  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 2200 Sand Hill Road, Suite 100  
; CITY: Menlo Park  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/660,626  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Valeta Gregg  
; REGISTRATION NUMBER: 35,127  
; REFERENCE/DOCKET NUMBER: 07532/003001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 322-5070  
; TELEFAX: (415) 854-0875  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 42 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; US-08-660-626-13

Query Match 2.0%; Score 21.2; DB 1; Length 42;  
Best Local Similarity 69.0%; Pred. No. 6.8e+02;  
Matches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 540 CCCATCTGTCTTGACCGCATTTGAGCTGAGGCCAATCAAT 581  
Db 1 CCTCCAGGCTTTGGCCGCTTTCGACGAGCCCTACATCACT 42

RESULT 2  
US-09-031-168-13  
; Sequence 13, Application US/09031168  
; Patent No. 6150583  
; GENERAL INFORMATION:  
; APPLICANT: Stanley B. Prusiner  
; APPLICANT: Glenn C. Telling  
; APPLICANT: Fred E. Cohen  
; APPLICANT: Michael R. Scott  
; TITLE OF INVENTION: TRANSGENIC ANIMALS EXPRESSING  
; TITLE OF INVENTION: EPIPOPE-TAGGED PROTEINS  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 2200 Sand Hill Road, Suite 100  
; CITY: Menlo Park  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/031,168  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/660,626  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Valeta Gregg  
; REGISTRATION NUMBER: 35,127  
; REFERENCE/DOCKET NUMBER: 07532/003001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 322-5070  
; TELEFAX: (415) 854-0875  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 42 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; US-09-031-168-13

Query Match 2.0%; Score 21.2; DB 3; Length 42;  
Best Local Similarity 69.0%; Pred. No. 6.8e+02;  
Matches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 540 CCCATCTGTCTTGACCGCATTTGAGCTGAGGCCAATCAAT 581  
Db 1 CCTCCAGGCTTTGGCCGCTTTCGACGAGCCCTACATCACT 42

RESULT 3  
US-08-860-882A-8  
; Sequence 8, Application US/08860882A  
; Patent No. 5985281  
; GENERAL INFORMATION:  
; APPLICANT: TAYLORSON, CHRISTOPHER JOHN  
; APPLICANT: EGGETTE, HENDRIKUS JOHANNES  
; APPLICANT: TARRAGONA-FIOL, ANTONIO

APPLICANT: RABIN, BRIAN ROBERT  
APPLICANT: BOYLE, FRANCIS THOMAS  
APPLICANT: HENNAM, JOHN FREDERICK  
APPLICANT: BLAKELY, DAVID CHARLES  
APPLICANT: MARSHAM, PETER ROBERT  
APPLICANT: HEATON, DAVID WILLIAM  
APPLICANT: DAVIES, DAVID HOW  
TITLE OF INVENTION: CHEMICAL COMPOUNDS  
NUMBER OF SEQUENCES: 77  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PILLSBURY, MADISON & SUTRO  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/860,882A  
FILING DATE: JUNE 23, 1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: DONALD J. BIRD  
REGISTRATION NUMBER: 25,323  
REFERENCE/DOCKET NUMBER: 9901/238653  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3027  
TELEFAX: (202) 822-0944  
TELEX: 6174627 CUSH  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-860-882A-8

Query Match 1.9%; Score 20.6; DB 2; Length 45;  
Best Local Similarity 85.2%; Pred. No. 1.1e+03;  
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 807 TGGTCGATGTGGCCTGACCTGG 833  
Db 19 TGGTCGCTTGTGCTGCTGCTGG 45

RESULT 4  
US-08-483-415-29/c  
Sequence 29, Application US/08483415  
Patent No. 5739409  
GENERAL INFORMATION:  
APPLICANT: FISCHER, ROBERT  
APPLICANT: KIM, SUNG-HO  
APPLICANT: CHO, JOONG M.  
APPLICANT: PENARRUBIA, LOLA  
APPLICANT: GIOVANNONI, JAMES  
APPLICANT: KIM, ROSALIND  
TITLE OF INVENTION: ENDOGENOUSLY SWEETENED TRANSGENIC PLANT  
TITLE OF INVENTION: PRODUCTS  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 PENNSYLVANIA AVENUE, NW  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,415  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MORASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 2000-0501.10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030 MRSNFOERSWSH  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-483-415-29

Query Match 1.9%; Score 20.2; DB 1; Length 45;  
Best Local Similarity 68.3%; Pred. No. 1.5e+03;  
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 392 AGGCAACATTTATGTCACCTAAGTGATGACATCAAA 432  
Db 44 AGAAACAGATTGTCATATGTGTAGATTGACTTCAACA 4

RESULT 5  
5487983-26/c  
Patent No. 5487983  
APPLICANT: KIM, SUNG-HOU; CHO, JOONG M.  
TITLE OF INVENTION: EXPRESSION SYSTEMS FOR MAKING  
SINGLE-CHAIN MONOMERIN ANALOGS  
NUMBER OF SEQUENCES: 36  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/146,326  
FILING DATE: 02-NOV-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 502,257  
FILING DATE: 30-MAY-1990  
APPLICATION NUMBER: 465,585  
FILING DATE: 18-JAN-1990  
APPLICATION NUMBER: 117,124  
FILING DATE: 04-NOV-1987  
APPLICATION NUMBER: 64,341  
FILING DATE: 19-JUN-1987  
APPLICATION NUMBER: 64,343  
FILING DATE: 19-JUN-1987  
SEQ ID NO: 26:  
LENGTH: 45  
5487983-26

Query Match 1.9%; Score 20.2; DB 6; Length 45;  
Best Local Similarity 68.3%; Pred. No. 1.5e+03;  
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 392 AGGCAACATTTATGTCACCTAAGTGATGACATCAAA 432  
Db 44 AGAAACAGATTGTCATATGTGTAGATTGACTTCAACA 4

RESULT 6  
US-08-985-162-1708  
Sequence 1708, Application US/08985162  
Patent No. 6057156  
GENERAL INFORMATION:  
APPLICANT: Akhtar, Saghir  
APPLICANT: Fell, Patricia

```

APPLICANT : MCSWIGGEN, JAMES
TITLE OF INVENTION : ENZYMATIC NUCLEIC ACID TREATMENT
TITLE OF INVENTION : OF DISEASES OR CONDITIONS RELATED
TITLE OF INVENTION : TO LEVELS OF EPIDERMAL GROWTH
TITLE OF INVENTION : FACTOR RECEPTORS
NUMBER OF SEQUENCES : 1877
CORRESPONDENCE ADDRESS :
ADDRESSEE : Lyon & Lyon
STREET : 633 West Fifth Street
CITY : Los Angeles
STATE : California
COUNTRY : U.S.A.
ZIP : 90071-2066
COMPUTER READABLE FORM :
MEDIUM TYPE : 3.5" Diskette, 1.44 Mb
MEDIUM TYPE : storage
COMPUTER : IBM compatible
OPERATING SYSTEM : IBM P.C. DOS 5.0
SOFTWARE : FASTSEQ for Windows 2.0
CURRENT APPLICATION DATA :
APPLICATION NUMBER : US/08/985,162
FILING DATE : 04 December 1997
CLASSIFICATION : 514
PRIOR APPLICATION DATA :
APPLICATION NUMBER : 60/036,476
FILING DATE : 31 January 1997
ATTORNEY/AGENT INFORMATION :
NAME : Warburg, Richard J.
REGISTRATION NUMBER : 32,327
REFERENCE/DOCKET NUMBER : 230/107
TELECOMMUNICATION INFORMATION :
TELEPHONE : (213) 489-1600
TELEX : (213) 955-0440
FAX : 67-3510
INFORMATION FOR SEQ ID NO : 1708 :
SEQUENCE CHARACTERISTICS :
LENGTH : 50 base pairs
TYPE : nucleic acid
STRANDEDNESS : single
TOPOLOGY : linear
US-08-985-162-1708

Query Match           1.9% ; Score 20.2; DB 3; Length 50;
Best Local Similarity   46.9%; Pred No.1,7e+03;
Matches    23; Conservative      8; Mismatches     18; Indels       0; Gaps         0.

          722 CAGCTGCCAAGCTACTGACGACATGTGGTGCATGTGCTGTT 770
             ||| - | ||| - | - | - | |||| - :: - | - | - |::|
        1 CAGUGAGAAGGUAAACACAGAAACACAGUUGUGUACAUAUCCUGU 49

RESULT 7
US-08-441-591-60/c
Sequence 60, Application US/08441591
Patent No. 5637682
GENERAL INFORMATION:
APPLICANT : NIEWMANDT, D., GOLD, L. AND WECKER, M.
TITLE OF INVENTION : HIGH-AFFINITY
TITLE OF INVENTION : OLIGONUCLEOTIDE LIGANDS
TITLE OF INVENTION : TO THE TACHYRININ
TITLE OF INVENTION : SUBSTANCE P
NUMBER OF SEQUENCES : 66
CORRESPONDENCE ADDRESS :
ADDRESSEE : Swanson & Bratschun, L.L.C.
STREET : 8400 E. Prentice Avenue, Suite 200
CITY : Englewood
STATE : Colorado
COUNTRY : USA
ZIP : 80111
COMPUTER READABLE FORM :
MEDIUM TYPE : Diskette, 3.50 inch, 1.44 MG storage
COMPUTER : IBM compatible

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1 OPERATING SYSTEM: MS-DOS
2 SOFTWARE: Wordperfect 5.1
3 CURRENT APPLICATION DATA:
4 APPLICATION NUMBER: US/08/441,591
5 FILING DATE:
6 CLASSIFICATION: 435
7 PRIOR APPLICATION DATA:
8 APPLICATION NUMBER: 08/303,362
9 FILING DATE: 9-SEPTEMBER-1994
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: 07/714,131
12 FILING DATE: 10-JUNE-1991
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: 07/931,473
15 FILING DATE: 17-AUGUST-1992
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: 08/117,991
18 FILING DATE: 8-SEPTEMBER 1993
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: 07/536,428
21 FILING DATE: 11-JUNE-1990
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: 07/964,624
24 FILING DATE: 21-OCTOBER-1992
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Barry J. Swanson
27 REGISTRATION NUMBER: 33,215
28 REFERENCE/DOCKET NUMBER: NEX21/C
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: (303) 793-3333
31 TELEFAX: (303) 793-3433
32 INFORMATION FOR SEQ ID NO: 60:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 47
35 TYPE: nucleic acid
36 STRANDEDNESS: single
37 TOPOLOGY: linear
38
39 US-08-441-591-60
40
41 Query Match 1.8%; Score 19.4; DB 1; Length 47;
42 Best Local Similarity 54.1%; Pred. No. 3e+03; 8; Indels 0; Gaps 0;
43 Matches 20; Conservative 9; Mismatches 3
44
45 QY 357 TGACGCATCAAAATTGCACAGTGTGATGCTGTGAG 393
46 1-||||| 11 :::: 1111 11 1 1111
47 DB 39 TTRACTGCTCCWDMWMMHMGSTGTCGTCTTTTGAG 3
48
49 RESULT 8
50 US-08-303-362A--60/C
51 Sequence 60, Application US/08303362A
52 Patent No. 5648214
53 GENERAL INFORMATION:
54 APPLICANT: NIEWIANDT, D., GOLD, L. AND WECKER, M.
55 TITLE OF INVENTION: HIGH-AFFINITY
56 TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
57 TITLE OF INVENTION: TO THE TACHYKININ
58 TITLE OF INVENTION: SUBSTANCE P
59 NUMBER OF SEQUENCES: 66
60 CORRESPONDENCE ADDRESS:
61 ADDRESSEE: Swanson & Bratschun, L.L.C.
62 STREET: 8400 E. Prentice Avenue, Suite 200
63 CITY: Englewood
64 STATE: Colorado
65 COUNTRY: USA
66 ZIP: 80111
67
68 COMPUTER READABLE FORM:
69 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
70 COMPUTER: IBM compatible
71 OPERATING SYSTEM: MS-DOS
72 SOFTWARE: Wordperfect 5.1
73 CURRENT APPLICATION DATA:
74 APPLICATION NUMBER: US/08/303,362A
75

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FILING DATE: 9-SEPTEMBER-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/714,131  
FILING DATE: 10-JUNE-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/931,473  
FILING DATE: 17-AUGUST-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/117,991  
FILING DATE: 8-SEPTEMBER-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/536,428  
FILING DATE: 11-JUNE-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/964,624  
FILING DATE: 21-OCTOBER-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEX21  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 60:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 47  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-303-362A-60

Query Match 1.8%; Score 19.4; DB 1; Length 47;  
Best Local Similarity 54.1%; Pred. No. 3e+03;  
Matches 20; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 357 TGAAGTCATCAATTTCACAGTGTGATGTTGAG 393  
DB 39 TAACTCGTCMDMWMHMGTCCTCTTTTGTGAG 3

RESULT 9  
PCT-US95-05600-77/c  
Sequence 77, Application PC/TUS9505600  
GENERAL INFORMATION:  
APPLICANT: GOLD, LARRY  
APPLICANT: NIEGLANDT, DAN  
APPLICANT: WECKER, MATTHEW  
APPLICANT: SCHNEIDER, DANIEL J.  
APPLICANT: FEIGON, JULI  
APPLICANT: ALLEN, PATRICK  
APPLICANT: SULLENGER, BRUCE A.  
APPLICANT: DOUDNA, JENNIFER, A.  
TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF  
TITLE OF INVENTION: INSULIN RECEPTOR ANTIBODIES, TACHYKININ SUBSTANCE  
TITLE OF INVENTION: P, HIV INTEGRASE AND HIV-1 REVERSE TRANSCRIPTASE  
NUMBER OF SEQUENCES: 239  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG  
MEDIUM TYPE: storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/05600  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/238,863  
FILING DATE: 06-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/248,632  
FILING DATE: 24-MAY-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/303,362  
FILING DATE: 09-SEPTEMBER-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/361,795  
FILING DATE: 21-DECEMBER-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/117,991  
FILING DATE: 08-SEPTEMBER-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/931,473  
FILING DATE: 17-AUGUST-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/964,624  
FILING DATE: 21-OCTOBER-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/536,428  
FILING DATE: 11-JUNE-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/714,131  
FILING DATE: 10-JUNE-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/536,428  
FILING DATE: 11-JUNE-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEX17/PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 77:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 47 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
PCT-US95-05600-77

Query Match 1.8%; Score 19.4; DB 5; Length 47;  
Best Local Similarity 54.1%; Pred. No. 3e+03;  
Matches 20; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 357 TGAAGTCATCAATTTCACAGTGTGATGTTGAG 393  
DB 39 TAACTCGTCMDMWMHMGTCCTCTTTTGTGAG 3

RESULT 10  
US-08-009-265-19  
Sequence 19, Application US/08009265  
Patent No. 5547871  
GENERAL INFORMATION:  
APPLICANT: Black Dr., Bruce C.  
APPLICANT: Summers Dr., Max D.  
TITLE OF INVENTION: Heterologous Signal Sequences For  
TITLE OF INVENTION: Secretion of Insect Controlling Proteins  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: 1937 West Main Street, P.O. Box 60  
CITY: Stamford  
STATE: CT  
COUNTRY: USA

ZIP: 06904-0060  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/009,265  
 FILING DATE: 19930125  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Gordon Mr., Alan M.  
 REGISTRATION NUMBER: 30637  
 REFERENCE/DOCKET NUMBER: 31868-00  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 203-321-2719  
 TELEFAX: 203-321-2971  
 TELE: 710-474-4059  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 48 base pairs  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Drosophila melanogaster  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..48  
 OS-08-009-265-19

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Query Match          1.8%; Score 19.2; DB 1; Length 48;
Best Local Similarity 62.5%; Pred. No. 3.5e+03;
Matches 30; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

0Y      989  ATGTTCAGTGTGTGATGAGTGATACACCAATGCGCGTGTTC 1036
          ||||| | | | | | | | | | | | | | | | | | |
Db      1  ATGTTCAGTTTGTTCATGATCGCCGACGTGTGGCGCTGGCGGTGCC 48

RESULT 11
PCT-US94-06079-40
; Sequence 40, Application PC/TUS9406079
GENERAL INFORMATION:
APPLICANT: American Cyanamid Company,
TITLE OF INVENTION: Gene Insertion by Direct Ligation In
TITLE OF INVENTION: Vitro
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: USA
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06079
FILING DATE: 27-MAY-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gordon, Alan M.
REGISTRATION NUMBER: 30,637
REFERENCE/DOCKET NUMBER: 31965-00\PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3244

```

TELEFAX: 201-831-3305  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
DCT-US94-06079-40

Query Match	1.8%;	Score 19.2;	DB 5;	Length 46;
Best Local Similarity	62.5%;	Pred. No. 3.5e+03;		
Matches	30;	Conservative	0;	Mismatches 18;
			Indels	0;
			Gaps	0;

QY 989 ATGTTTCATGTGTGTGAAGGTGTACAGCAATGGCGGTGTGTTCTCC 1036  
||||| ||||| ||||| ||||| |||||  
Db 1 ATGTTTCAGTGTGTGATGATCTGCCGAGTTTTGGGCCTGGCGGTGCC 48

RESULT 12  
US-08-864-473-10/c  
; Sequence 10, Application US/08864473

```

1  GENERAL INFORMATION:
2  APPLICANT: Barany, Francis
3  APPLICANT: Lublin, Matthew
4  TITLE OF INVENTION: DETECTION OF NUCLEIC ACID SEQUENCE DIFFERENCES USING
5  TITLE OF INVENTION: COUPLED LIGASE DETECTION AND POLYMERASE CHAIN REACTIONS
6  FILE REFERENCE: 19603/441
7  CURRENT APPLICATION NUMBER: US/08/864,473
8  CURRENT FILING DATE: 1997-05-28
9  EARLIER APPLICATION NUMBER: 60/018,532
10 EARLIER FILING DATE: 1996-05-29
11 NUMBER OF SEQ ID NOS: 76
12 SOFTWARE: PatentIn Ver. 2.0
13 SEQ ID NO 10
14 LENGTH: 47
15 TYPE: DNA
16 ORGANISM: Artificial Sequence
17 FEATURE:
18 OTHER INFORMATION: Description of Artificial Sequence: Probe
19 US-08-864-473-10

```

Query Match	1.7%;	Score 19;	DB 3;	Length 47;
Best Local Similarity	65.1%;	Pred. No. 4e+03;		
Matches 28; Conservative	0;	Mismatches 15;	Indels 0;	Gaps 0;

QY 614 ATCAACAGCTCTATGACAATGGTCTTCACAGTTTGTGATGA 656  
| | | | | | | | | | | | | | |  
Db 44 AACTACCGACTATTGTAGCGGCCACCAGTCTTTTCTGATAGA 2

```

1      RESULT 13
2      US-09-440-523-10/C
3      ; Sequence 10, Application US/09440523
4      ; Patent No. 6268148
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Barany, Francis
7      ; APPLICANT: Lublin, Matthew
8      ; TITLE OF INVENTION: DETECTION OF NUCLEIC ACID SEQUENCE DIFFERENCES USING
9      ; TITLE OF INVENTION: COUPLED LIGASE DETECTION AND POLYMERASE CHAIN REACTIONS
10     ; FILE REFERENCE: 19603/441
11     ; CURRENT APPLICATION NUMBER: US/09/440,523
12     ; CURRENT FILING DATE: 1999-11-15
13     ; PRIOR APPLICATION NUMBER: 08/864,473
14     ; PRIOR FILING DATE: 1997-05-28
15     ; NUMBER OF SEQ ID NOS: 76
16     ; SOFTWARE: PatentIn Ver. 2.0
17     ; SEQ ID NO 10
18     ; LENGTH: 47

```

TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Probe  
US-09-440-523-10

Query Match  
Best Local Similarity 65.1%; Score 19; DB 4; Length 47;  
Matches 28; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

DB 614 ATCAACAGCTATGCAATGTCCTTCCAGGTTTGTGATGA 656  
44 AACTACCGCATATGAGCGCCACCGCTTTTCTGATAGA 2

RESULT 14  
US-08-998-099-298  
Sequence 298, Application US/08998099A  
Patent No. 6103890  
GENERAL INFORMATION:  
APPLICANT: JARVIS, THALE  
APPLICANT: MCSWIGEN, JAMES A.  
APPLICANT: STINCHCOMB, DAN T.  
TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT OF DISEASES  
FILE REFERENCE: 231/175  
CURRENT APPLICATION NUMBER: US/08/998, 099A  
CURRENT FILING DATE: 1997-12-24  
EARLIER APPLICATION NUMBER: 60/037, 658  
EARLIER FILING DATE: 1997-01-23  
EARLIER APPLICATION NUMBER: 08/373, 124  
EARLIER FILING DATE: 1995-01-13  
EARLIER APPLICATION NUMBER: 08/245, 466  
EARLIER FILING DATE: 1994-05-18  
NUMBER OF SEQ ID NOS: 375  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 298  
LENGTH: 50  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthesized Hairpin Ribozyme  
US-08-998-099-298

Query Match  
Best Local Similarity 1.7%; Score 18.8; DB 3; Length 50;  
Matches 22; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

DB 725 CTGCCAGCTAGTACTGAGCAGCATGTTGTCATGTCGTGT 770  
4 CUGAGACGACGACGACGAGAACACACGUGUGUACAUUACCUUGU 49

RESULT 15  
US-09-026-276-8  
Sequence 8, Application US/09026276  
Patent No. 6319503  
GENERAL INFORMATION:  
APPLICANT: Kenten, John H  
APPLICANT: Trimontano, Alfonso  
APPLICANT: Pilon, April L  
APPLICANT: Lohmas, Gerald L  
APPLICANT: Roberts, Steven F  
TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM  
FILE REFERENCE: U.S. Patent Application No. 6319503 09/026,276  
CURRENT FILING DATE: 1998-02-19  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 8  
LENGTH: 50  
TYPE: DNA

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: cloning oligo  
US-09-026-276-8

Query Match  
Best Local Similarity 1.7%; Score 18.8; DB 4; Length 50;  
Matches 29; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

DB 845 AGACGCGCTGAGGCTTCCCGTCGACATGTCGCGCGGCTCG 890  
3 AAGACTGGCTGGCGCTGACGACGATTCCTTCACGCCCTGCGCGG 48

RESULT 16  
US-09-042-943-13  
Sequence 13, Application US/09042943  
Patent No. 6218128  
GENERAL INFORMATION:  
APPLICANT: KLEIN, ELLIOTT S.  
APPLICANT: JOHNSON, ALAN T.  
APPLICANT: STANDEVEN, ANDREW M.  
APPLICANT: BEARD, RICHARD L.  
APPLICANT: GILLET, SAMUEL J.  
APPLICANT: DUONG, TIEN T.  
APPLICANT: NAGPAL, SUNIL  
APPLICANT: VULIGONDA, VIDYASAGAR  
APPLICANT: TENG TENG, MIN  
APPLICANT: CHANDRARATNA, ROSHANTHA A.  
TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS  
TITLE OF INVENTION: HAVING NUCLEAR RECEPTOR NEGATIVE HORMONE AND/OR ANTAGONIST  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Allergan, Inc.  
STREET: 2525 Dupont Drive  
CITY: Irvine  
STATE: CA  
COUNTRY: USA  
ZIP: 92623  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/042,943  
FILING DATE: 16-MAR-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/928,552  
FILING DATE: 12-SEP-1997  
APPLICATION NUMBER: 08/613,863  
FILING DATE: 11-MAR-1997  
APPLICATION NUMBER: 08/542,648  
FILING DATE: 13-OCT-1995  
APPLICATION NUMBER: 08/522,779  
FILING DATE: 01-SEP-1995  
APPLICATION NUMBER: 08/522,778  
FILING DATE: 01-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Fisher, Carlos A  
REGISTRATION NUMBER: 36,510  
REFERENCE/DOCKET NUMBER: 1717CIP4 (HL)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 714-246-4920  
TELEFAX: 714-246-4249  
TELEX:  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-09-042-943-13

Query Match 1.7%; Score 18.6; DB 4; Length 28;  
Best Local Similarity 84.0%; Pred. No. 3.9e+03;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 652 ATGATGTTGTCAGCCTAGGACT 676  
||||| ||||| |||||  
DB 3 ATGATCTGTGTCAGCCTGGGACT 27

RESULT 17  
US-08-437-841-28  
Sequence 28, Application US/08437841  
Patent No. 5563123  
GENERAL INFORMATION:

APPLICANT: Innis, Michael  
TITLE OF INVENTION: Chimeric Proteins  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton St.  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/437,841  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/286,521  
FILING DATE: 05-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Saveriede, Paul B.  
REGISTRATION NUMBER: 36,914  
REFERENCE/DOCKET NUMBER: 0990.001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-601-2585  
TELEFAX: 510-655-3542

INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer"  
US-08-437-841-28

Query Match 1.7%; Score 18.6; DB 1; Length 34;  
Best Local Similarity 72.7%; Pred. No. 4.4e+03;  
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 510 CAAGTCAATGCTGGATTACTACTGACCC 542  
||||| ||||| ||||| |||||  
DB 1 CCAGCTCAATGCTGTGATAAATCTCCCTGACTCC 33

RESULT 18  
US-08-286-521-28  
Sequence 28, Application US/08286521  
Patent No. 5589359  
GENERAL INFORMATION:  
APPLICANT: Innis, Michael

APPLICANT: Creasey, Abia  
TITLE OF INVENTION: Chimeric Proteins  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton St.  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/286,521  
FILING DATE: 05-AUG-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Saveriede, Paul B.  
REGISTRATION NUMBER: 36,914  
REFERENCE/DOCKET NUMBER: 0990.001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-601-2585  
TELEFAX: 510-655-3542

INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer"  
US-08-286-521-28

Query Match 1.7%; Score 18.6; DB 1; Length 34;  
Best Local Similarity 72.7%; Pred. No. 4.4e+03;  
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 510 CAAGTCAATGCTGGATTACTACTGACCC 542  
||||| ||||| ||||| |||||  
DB 1 CCAGCTCAATGCTGTGATAAATCTCCCTGACTCC 33

RESULT 19  
US-08-436-175-28  
Sequence 28, Application US/08436175  
Patent No. 5696088  
GENERAL INFORMATION:

APPLICANT: Innis, Michael  
TITLE OF INVENTION: Chimeric Proteins  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton St.  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/436,175  
FILING DATE: 09-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,521  
FILING DATE: 05-AUG-1994



ATTORNEY/AGENT INFORMATION:  
NAME: Saveriede, Paul B.  
REGISTRATION NUMBER: 36,914  
REFERENCE/DOCKET NUMBER: 0990.001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-601-2585  
TELEFAX: 510-655-3542  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer"  
US-08-436-175-28

Query Match 1.7%; Score 18.6; DB 1; Length 34;  
Best Local Similarity 72.7%; Pred. No. 4.4e+03;  
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 1 510 CAGATCAATGCTGGATTCTTACTTCTGAACCC 542  
1 CCAAGCTCAATGCTGTGAATACTCTCCCTGACTCC 33

RESULT 20  
US-08-943-682-28  
Sequence 28, Application US/08943682  
Patent No. 6174/21  
GENERAL INFORMATION:  
APPLICANT: Innis, Michael  
APPLICANT: Creasey, Adla  
TITLE OF INVENTION: Chimeric Proteins  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton St.  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,682  
FILING DATE: 03-OCT-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/438,184  
FILING DATE: 09-MAY-1995  
APPLICATION NUMBER: US 08/286,521  
FILING DATE: 05-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Saveriede, Paul B.  
REGISTRATION NUMBER: 36,914  
REFERENCE/DOCKET NUMBER: 0990.001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-601-2585  
TELEFAX: 510-655-3542  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer"  
US-08-943-682-28

Query Match 1.7%; Score 18.6; DB 4; Length 34;  
Best Local Similarity 72.7%; Pred. No. 4.4e+03;  
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 510 CAGATCAATGCTGGATTCTTACTTCTGAACCC 542  
Db 1 CCAAGCTCAATGCTGTGAATACTCTCCCTGACTCC 33

RESULT 21  
PCT-US95-09464-28  
Sequence 28, Application PC/TUS9509464  
GENERAL INFORMATION:  
APPLICANT: CHIRON CORPORATION  
TITLE OF INVENTION: Chimeric Proteins  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton St.  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/09464  
FILING DATE: 25-JULY-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Saveriede, Paul B.  
REGISTRATION NUMBER: 36,914  
REFERENCE/DOCKET NUMBER: 0990.100  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-601-2585  
TELEFAX: 510-655-3542  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer"  
PCT-US95-09464-28

Query Match 1.7%; Score 18.6; DB 5; Length 34;  
Best Local Similarity 72.7%; Pred. No. 4.4e+03;  
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 510 CAGATCAATGCTGGATTCTTACTTCTGAACCC 542  
Db 1 CCAAGCTCAATGCTGTGAATACTCTCCCTGACTCC 33

RESULT 22  
US-08-406-855A-9  
Sequence 9, Application US/08406855A  
Patent No. 5861309  
GENERAL INFORMATION:  
APPLICANT: Jonathan A. Bard et al.  
TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrennergic  
RECEPTORS AND USES THEREOF  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.

ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/406,855A  
FILING DATE: 21-Aug-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41337-A-PCT-US/JPW/KDB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0526  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-406-855A-9

Query Match 1.7%; Score 18.6; DB 2; Length 45;  
Best Local Similarity 65.9%; Pred. No. 5.4e+03;  
Matches 27; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 135 GGTACAGAGTGGTTTGGCTATCACTATCCGCCAGAG 175  
DB 5 GGCTCCGAGTGGTGTGCGCATCCACTGTCCGGCGCG 45

RESULT 23  
US-09-206-899-9  
Sequence 9, Application US/09206899  
Patent No. 6083705  
GENERAL INFORMATION:  
APPLICANT: Jonathan A. Bard et al.  
TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic  
TITLE OF INVENTION: Receptors and Uses Thereof  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/206,899  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/406,855  
FILING DATE: 21-Aug-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41337-A-PCT-US/JPW/KDB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0526  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-206-899-9

Query Match 1.7%; Score 18.6; DB 3; Length 45;  
Best Local Similarity 65.9%; Pred. No. 5.4e+03;  
Matches 27; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 135 GGTACAGAGTGGTTTGGCTATCACTATCCGCCAGAG 175  
DB 5 GGCTCCGAGTGGTGTGCGCATCCACTGTCCGGCGCG 45

RESULT 24  
US-08-715-568A-6  
Sequence 6, Application US/08715568A  
Patent No. 5856463  
GENERAL INFORMATION:  
APPLICANT: Prydz, Hans Peter Blankenborg  
APPLICANT: Breda, Gaute  
TITLE OF INVENTION: psKH-1 Ribozymes and Uses in Disease  
TITLE OF INVENTION: Treatment  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik  
STREET: 600 South Avenue West  
CITY: Westfield  
STATE: NJ  
COUNTRY: USA  
ZIP: 07090-1497  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/715,568A  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Foley, Shawn P.  
REFERENCE/DOCKET NUMBER: FORSK 3.0-002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-654-5000  
TELEFAX: 908-654-7866  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: both  
US-08-715-568A-6

Query Match 1.7%; Score 18.6; DB 2; Length 50;  
Best Local Similarity 46.9%; Pred. No. 5.8e+03;  
Matches 23; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

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DB 1 CAGCTGCCAGTACTACTGAGCAGCATGTGTGGCAATGTGCTGT 49

RESULT 25  
US-08-985-162-1663  
Sequence 1663, Application US/08985162  
Patent No. 6057156  
GENERAL INFORMATION:  
APPLICANT: Akhtar, Saghir  
APPLICANT: Fell, Patricia  
APPLICANT: McSwiggen, James  
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT

1 TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED  
 2 TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH  
 3 TITLE OF INVENTION: FACTOR RECEPTORS  
 4 NUMBER OF SEQUENCES: 1877  
 5 CORRESPONDENCE ADDRESS:  
 6 ADDRESSEE: Lyon & Lyon  
 7 STREET: 633 West Fifth Street  
 8 STREET: Suite 4700  
 9 CITY: Los Angeles  
 10 STATE: California  
 11 COUNTRY: U.S.A.  
 12 ZIP: 90071-2066  
 13  
 14 COMPUTER READABLE FORM:  
 15 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 16 MEDIUM TYPE: storage  
 17 COMPUTER: IBM Compatible  
 18 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 19 SOFTWARE: FastSEO for Windows 2.0  
 20 CURRENT APPLICATION DATA:  
 21 APPLICATION NUMBER: US/08/985,162  
 22 FILING DATE: 04 December 1997  
 23 CLASSIFICATION: 514  
 24  
 25 PRIOR APPLICATION DATA:  
 26 APPLICATION NUMBER: 60/036,476  
 27 FILING DATE: 31 January 1997  
 28 ATTORNEY/AGENT INFORMATION:  
 29 NAME: Warburg, Richard J.  
 30 REGISTRATION NUMBER: 32,327  
 31 REFERENCE/DOCKET NUMBER: 230/107  
 32 TELECOMMUNICATION INFORMATION:  
 33 TELEPHONE: (213) 489-1600  
 34 TELEFAX: (213) 955-0440  
 35 TELEX: 67-3510  
 36  
 37 INFORMATION FOR SEQ. ID NO.: 1663:  
 38 SEQUENCE CHARACTERISTICS:  
 39 LENGTH: 50 base pairs  
 40 TYPE: nucleic acid  
 41 STRANDEDNESS: single  
 42 TOPOLOGY: linear  
 43  
 44 US-08-985-162-1663

	Query Match	1.7%	Score 18.6;	DB 3;	length 50;
	Best Local Similarity	48.8%;	Pred. No. 5,8e+03;		
	Matches	20;	Conservative	7;	Mismatches 14; Indels 0; Gaps 0;
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Search completed: October 22, 2002, 17:41:52  
Job time : 65 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: October 22, 2002, 14:22:31 : Search time 1546 Seconds

(without alignments)  
9481.043 Million cell updates/sec

Title: US-09-374-967-1

Perfect score: 1086

Sequence: 1 atgaagcccatctctgt.....agcctgagatcgtcatgtga 1086

Scoring table: IDENTITY NUC

Searched: 13736207 seqs, 6748477542 residues

Minimum DB seq length: 20  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST: \*  
1: em\_estb: \*  
2: em\_esth: \*  
3: em\_esti: \*  
4: em\_estm: \*  
5: em\_estov: \*  
6: em\_estpl: \*  
7: em\_estro: \*  
8: em\_hlc: \*  
9: gb\_estl: \*  
10: gb\_est2: \*  
11: gb\_hlc: \*  
12: gb\_gss: \*  
13: em\_gss\_hum: \*  
14: em\_gss\_inv: \*  
15: em\_gss\_pln: \*  
16: em\_gss\_vrl: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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9	18.6	1.7	38	10	R82106
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11	18.4	1.7	40	9	AU1080507
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C 238	16	1.5	50	9	AU102500	AU102500	C 311	15.8	1.5	50	12	BH624899	BH624899 1007089F0
C 239	16	1.5	50	9	AU102881	AU102881	C 312	15.8	1.5	50	12	TA300F120	TA300F120 T. brucei
240	16	1.5	50	9	AU103666	AU103666	313	15.6	1.4	31	12	A2979245	A2979245 2M0255D20
241	16	1.5	50	9	AU103798	AU103798	C 314	15.6	1.4	32	10	C21095	C21095 HUMS000261
242	16	1.5	50	9	AU104869	AU104869	C 315	15.6	1.4	32	12	A2784967	A2784967 2M02028H20
243	16	1.5	50	9	AU104998	AU104998	C 316	15.6	1.4	33	10	T64659	T64659 ycc25907.s1
244	16	1.5	50	9	AU105032	AU105032	C 317	15.6	1.4	37	9	AT6878791	AT6878791 oF82e05.s
245	16	1.5	50	9	AU105087	AU105087	C 318	15.6	1.4	37	9	AT6878791	AT6878791 oF82e05.s
C 246	16	1.5	50	9	AU106727	AU106727	C 319	15.6	1.4	37	10	H23949	H23949 y7f5f10.s1
C 248	16	1.5	50	9	AU106741	AU106741	C 320	15.6	1.4	37	10	A2845294	A2845294 t230d10.x
C 249	16	1.5	50	9	AU106989	AU106989	C 321	15.6	1.4	38	12	A2579427	A2579427 1M0363H23
C 250	16	1.5	50	9	AU106990	AU106990	C 322	15.6	1.4	40	9	AT6878791	AT6878791 oF82e05.s
C 251	16	1.5	50	10	BJ033164	BJ033164	C 323	15.6	1.4	40	9	AA485666	AA485666 qx91a07.s
C 252	16	1.5	50	12	A2473369	A2473369	C 324	15.6	1.4	40	12	A2784839	A2784839 2M02028C09
C 253	16	1.5	50	12	A263650	A263650	C 325	15.6	1.4	40	12	TA254A12P	TA254A12P T. brucei
C 254	15.8	1.5	28	9	AT826975	AT826975	C 326	15.6	1.4	41	12	A2340079	A2340079 1M0071A19
C 255	15.8	1.5	29	12	A2777445	A2777445	C 327	15.6	1.4	41	12	A2662472	A2662472 1M00541A09
C 256	15.8	1.5	34	12	A2510095	A2510095	C 328	15.6	1.4	41	12	A2992328	A2992328 2M0276N21
C 257	15.8	1.5	35	12	A2816449	A2816449	C 329	15.6	1.4	42	12	TA386040	TA386040 T. brucei
C 258	15.8	1.5	36	12	A2623431	A2623431	C 330	15.6	1.4	42	12	A2312977	A2312977 1M0029F07
C 259	15.8	1.5	37	9	AA920462	AA920462	C 331	15.6	1.4	43	12	A2795823	A2795823 2M0051E13
C 260	15.8	1.5	37	9	AA929493	AA929493	C 332	15.6	1.4	43	9	AA862169	AA862169 o148h04.s
C 261	15.8	1.5	37	10	BM008282	BM008282	C 333	15.6	1.4	43	12	A2788733	A2788733 2M0036M03
C 262	15.8	1.5	39	10	BJ081377	BJ081377	C 334	15.6	1.4	45	12	A2454306	A2454306 1M0256C08
C 263	15.8	1.5	39	12	A2997025	A2997025	C 335	15.6	1.4	46	9	HSM010239	HSM010239 Homo sapi
C 264	15.8	1.5	40	9	AT941418	AT941418	C 336	15.6	1.4	46	9	AA936328	AA936328 oF87a05.s
C 265	15.8	1.5	40	12	A2378558	A2378558	C 337	15.6	1.4	46	10	T56929	T56929 ya83f08.r2
C 266	15.8	1.5	40	12	A2410396	A2410396	C 338	15.6	1.4	46	12	BH623606	BH623606 1007080A0
C 267	15.8	1.5	40	12	A2816635	A2816635	C 339	15.6	1.4	47	12	A2786403	A2786403 2M0031G20
268	15.8	1.5	41	12	A2793879	A2793879	C 340	15.6	1.4	47	12	A2843553	A2843553 2M0142A03
269	15.8	1.5	41	12	BH629902	BH629902	C 341	15.6	1.4	48	10	BT756103	BT756103 603022994
270	15.8	1.5	43	9	AA917216	AA917216	C 342	15.6	1.4	48	12	A2800696	A2800696 2M0058B21
271	15.8	1.5	43	10	BT769957	BT769957	C 343	15.6	1.4	48	12	A2816555	A2816555 2M0110K18
C 272	15.8	1.5	43	10	A2317179	A2317179	C 344	15.6	1.4	48	12	A2830843	A2830843 2M0110K18
C 273	15.8	1.5	44	10	T84465	T84465	C 345	15.6	1.4	49	9	AA649346	AA649346 z686f11.s
C 274	15.8	1.5	44	12	A2393428	A2393428	C 346	15.6	1.4	49	9	AA025722	AA025722 z686f11.s
C 275	15.8	1.5	45	9	AV833594	AV833594	C 347	15.6	1.4	49	9	AA649346	AA649346 z686f11.s
C 276	15.8	1.5	45	12	A2507560	A2507560	C 348	15.6	1.4	49	9	AT032978	AT032978 ox22D01.s
C 277	15.8	1.5	46	9	AA916623	AA916623	C 349	15.6	1.4	49	9	AT141486	AT141486 ma08f03.x
C 278	15.8	1.5	46	12	BG436954	BG436954	C 350	15.6	1.4	49	9	AT1917385	AT1917385 ts83h12.x
C 279	15.8	1.5	47	10	A2511408	A2511408	C 351	15.6	1.4	49	12	A2827730	A2827730 mv93b08.r
C 280	15.8	1.5	47	12	A2587378	A2587378	C 352	15.6	1.4	50	9	AA207982	AA207982 2M0104O17
C 281	15.8	1.5	47	12	A2587378	A2587378	C 353	15.6	1.4	50	9	AT103392	AT103392 1679 Pine
C 282	15.8	1.5	48	12	A2834843	A2834843	C 354	15.6	1.4	50	9	AT103392	AT103392 1679 Pine
C 283	15.8	1.5	49	9	AA780186	AA780186	C 355	15.6	1.4	50	9	AT103392	AT103392 1679 Pine
C 284	15.8	1.5	49	9	AA870321	AA870321	C 356	15.6	1.4	50	9	AT103392	AT103392 1679 Pine
C 285	15.8	1.5	49	9	AA870321	AA870321	C 357	15.6	1.4	50	9	AT103392	AT103392 1679 Pine
286	15.8	1.5	49	9	AA870321	AA870321	C 358	15.6	1.4	50	9	AT103392	AT103392 1679 Pine
287	15.8	1.5	49	9	AA870321	AA870321	C 359	15.6	1.4	50	9	AT103392	AT103392 1679 Pine
C 288	15.8	1.5	49	9	AA870321	AA870321	C 360	15.6	1.4	50	9	AT103392	AT103392 1679 Pine
C 289	15.8	1.5	50	9	AA870321	AA870321	C 361	15.6	1.4	50	9	AT103392	AT103392 1679 Pine
C 290	15.8	1.5	50	9	AA870321	AA870321	C 362	15.6	1.4	50	9	AT103392	AT103392 1679 Pine
C 291	15.8	1.5	50	9	AA870321	AA870321	C 363	15.6	1.4	50	9	AT103392	AT103392 1679 Pine
C 292	15.8	1.5	50	9	AA870321	AA870321	C 364	15.6	1.4	50	9	AT103392	AT103392 1679 Pine
C 293	15.8	1.5	50	9	AA870321	AA870321	C 365	15.6	1.4	50	9	AT103392	AT103392 1679 Pine
C 294	15.8	1.5	50	9	AA870321	AA870321	C 366	15.6	1.4	50	9	AT103392	AT103392 1679 Pine
C 295	15.8	1.5	50	9	AA870321	AA870321	C 367	15.6	1.4	50	9	AT103392	AT103392 1679 Pine
C 296	15.8	1.5	50	9	AA870321	AA870321	C 368	15.6	1.4	50	9	AT103392	AT103392 1679 Pine
C 297	15.8	1.5	50	9	AA870321	AA870321	C 369	15.6	1.4	50	9	AT103392	AT103392 1679 Pine
C 298	15.8	1.5	50	9	AA870321	AA870321	C 370	15.6	1.4	50	9	AT103392	AT103392 1679 Pine
C 299	15.8	1.5	50	9	AA870321	AA870321	C 371	15.6	1.4	50	9	AT103392	AT103392 1679 Pine
C 300	15.8	1.5	50	9	AA870321	AA870321	C 372	15.6	1.4	50	9	AT103392	AT103392 1679 Pine
C 301	15.8	1.5	50	9	AA870321	AA870321	C 373	15.6	1.4	50	9	AT103392	AT103392 1679 Pine
C 302	15.8	1.5	50	9	AA870321	AA870321	C 374	15.6	1.4	50	9	AT103392	AT103392 1679 Pine
C 303	15.8	1.5	50	9	AA870321	AA870321	C 375	15.6	1.4	50	9	AT103392	AT103392 1679 Pine
C 304	15.8	1.5	50	9	AA870321	AA870321	C 376	15.6	1.4	50	9	AT103392	AT103392 1679 Pine
C 305	15.8	1.5	50	9	AA870321	AA870321	C 377	15.6	1.4	50	9	AT103392	AT103392 1679 Pine
C 306	15.8	1.5	50	9	AA870321	AA870321	C 378	15.6	1.4	50	9	AT103392	AT103392 1679 Pine
C 307	15.8	1.5	50	9	AA870321	AA870321	C 379	15.6	1.4	50	9	AT103392	AT103392 1679 Pine
C 308	15.8	1.5	50	9	AA870321	AA870321	C 380	15.6	1.4	50	9	AT103392	AT103392 1679 Pine
C 309	15.8	1.5	50	9	AA870321	AA870321	C 381	15.6	1.4	50	9	AT103392	AT103392 1679 Pine
							C 382	15.4	1.4	37	12	A2789783	A2789783 2M0037H19

C 383	15.4	1.4	38	10	BU084457	BU084457	C 456	15.4	1.4	50	9	AU104783	AU104783
C 384	15.4	1.4	39	10	BU045293	BU045293	C 457	15.4	1.4	50	9	AU104860	AU104860
C 385	15.4	1.4	39	12	AZ787448	AZ787448	C 458	15.4	1.4	50	9	AU104993	AU104993
C 386	15.4	1.4	40	9	AA034448	AA034448	C 459	15.4	1.4	50	9	AU105954	AU105954
C 387	15.4	1.4	40	9	AA872828	AA872828	C 460	15.4	1.4	50	9	AV845266	AV845266
C 388	15.4	1.4	40	12	AZ376869	AZ376869	C 461	15.4	1.4	50	10	TE62585	TE62585
C 389	15.4	1.4	40	12	AZ511081	AZ511081	C 462	15.4	1.4	50	10	BE882523	BE882523
C 390	15.4	1.4	41	12	AZ504919	AZ504919	C 463	15.4	1.4	50	12	AZ329369	AZ329369
C 391	15.4	1.4	41	12	AZ776402	AZ776402	C 464	15.4	1.4	50	12	AZ344153	AZ344153
C 392	15.4	1.4	41	12	BH614871	BH614871	C 465	15.4	1.4	50	12	AZ482876	AZ482876
C 393	15.4	1.4	42	12	AZ406514	AZ406514	C 466	15.4	1.4	50	12	AZ785734	AZ785734
C 394	15.4	1.4	42	12	AZ804215	AZ804215	C 467	15.2	1.4	28	12	AZ583628	AZ583628
C 395	15.4	1.4	42	12	TA87603P	TA87603P	C 468	15.2	1.4	28	12	AZ583628	AZ583628
C 396	15.4	1.4	43	9	A1457749	A1457749	C 469	15.2	1.4	30	12	AZ633504	AZ633504
C 397	15.4	1.4	43	12	AZ308202	AZ308202	C 470	15.2	1.4	31	9	A1032171	A1032171
C 398	15.4	1.4	43	12	AZ443922	AZ443922	C 471	15.2	1.4	34	10	BU050207	BU050207
C 399	15.4	1.4	43	12	AZ456311	AZ456311	C 472	15.2	1.4	36	12	AZ456364	AZ456364
C 400	15.4	1.4	43	12	AZ860401	AZ860401	C 473	15.2	1.4	36	12	AZ482686	AZ482686
C 401	15.4	1.4	44	9	AA613679	AA613679	C 474	15.2	1.4	37	9	AA908535	AA908535
C 402	15.4	1.4	44	10	BU033613	BU033613	C 475	15.2	1.4	37	9	A1354343	A1354343
C 403	15.4	1.4	44	12	AZ654523	AZ654523	C 476	15.2	1.4	37	10	B1080927	B1080927
C 404	15.4	1.4	44	12	AZ812365	AZ812365	C 477	15.2	1.4	37	12	AZ463628	AZ463628
C 405	15.4	1.4	44	12	TA188G090	TA188G090	C 478	15.2	1.4	38	12	AA247837	AA247837
C 406	15.4	1.4	45	10	B1685352	B1685352	C 479	15.2	1.4	38	12	AZ600409	AZ600409
C 407	15.4	1.4	45	10	C01976	C01976	C 480	15.2	1.4	39	10	AZ759713	AZ759713
C 408	15.4	1.4	45	12	AZ769215	AZ769215	C 481	15.2	1.4	39	10	B1001320	B1001320
C 409	15.4	1.4	45	12	TA78C100	TA78C100	C 482	15.2	1.4	39	12	AZ447242	AZ447242
C 410	15.4	1.4	46	9	AA938483	AA938483	C 483	15.2	1.4	39	12	A1021202	A1021202
C 411	15.4	1.4	46	9	A1441223	A1441223	C 484	15.2	1.4	40	9	A1021202	A1021202
C 412	15.4	1.4	46	10	TE63094	TE63094	C 485	15.2	1.4	40	9	A1747109	A1747109
C 413	15.4	1.4	47	10	AL641834	AL641834	C 486	15.2	1.4	40	9	AA220540	AA220540
C 414	15.4	1.4	47	10	B151478	B151478	C 487	15.2	1.4	40	9	AL641304	AL641304
C 415	15.4	1.4	47	10	H52206	H52206	C 488	15.2	1.4	40	12	AZ37182	AZ37182
C 416	15.4	1.4	47	12	AZ331661	AZ331661	C 489	15.2	1.4	40	12	TA37A090	TA37A090
C 417	15.4	1.4	47	12	AZ362217	AZ362217	C 490	15.2	1.4	41	12	AZ335333	AZ335333
C 418	15.4	1.4	47	12	AZ824937	AZ824937	C 491	15.2	1.4	41	12	AZ27747	AZ27747
C 419	15.4	1.4	48	10	B1456893	B1456893	C 492	15.2	1.4	41	12	AZ783895	AZ783895
C 420	15.4	1.4	48	10	B1456900	B1456900	C 493	15.2	1.4	42	10	B1040540	B1040540
C 421	15.4	1.4	48	10	U26151	U26151	C 494	15.2	1.4	42	10	C58084	C58084
C 422	15.4	1.4	48	12	AZ331196	AZ331196	C 495	15.2	1.4	42	12	AZ785478	AZ785478
C 423	15.4	1.4	48	12	AZ401474	AZ401474	C 496	15.2	1.4	42	12	AZ826326	AZ826326
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C 425	15.4	1.4	48	12	AZ785080	AZ785080	C 498	15.2	1.4	43	9	AA693121	AA693121
C 426	15.4	1.4	48	12	AZ819513	AZ819513	C 499	15.2	1.4	43	9	A1291844	A1291844
C 427	15.4	1.4	48	12	AZ927703	AZ927703	C 500	15.2	1.4	43	10	D67705	D67705
C 428	15.4	1.4	49	9	AA876193	AA876193	C 501	15.2	1.4	43	12	AZ848637	AZ848637
C 429	15.4	1.4	49	9	AA907913	AA907913	C 502	15.2	1.4	44	9	AA687683	AA687683
C 430	15.4	1.4	49	9	AA627247	AA627247	C 503	15.2	1.4	44	12	AZ448511	AZ448511
C 431	15.4	1.4	49	10	BM054834	BM054834	C 504	15.2	1.4	44	12	AZ787976	AZ787976
C 432	15.4	1.4	49	10	BM271488	BM271488	C 505	15.2	1.4	44	12	AZ808682	AZ808682
C 433	15.4	1.4	49	12	AZ492778	AZ492778	C 506	15.2	1.4	45	9	AV831108	AV831108
C 434	15.4	1.4	49	12	AZ641368	AZ641368	C 507	15.2	1.4	45	12	AZ648348	AZ648348
C 435	15.4	1.4	49	12	AZ771655	AZ771655	C 508	15.2	1.4	45	12	AZ768397	AZ768397
C 436	15.4	1.4	49	12	AZ805592	AZ805592	C 509	15.2	1.4	45	12	AZ824418	AZ824418
C 437	15.4	1.4	49	12	CNS0VF2V	CNS0VF2V	C 510	15.2	1.4	46	9	AA828900	AA828900
C 438	15.4	1.4	50	9	AU102271	AU102271	C 511	15.2	1.4	46	9	AA903146	AA903146
C 439	15.4	1.4	50	9	AU102297	AU102297	C 512	15.2	1.4	46	9	A1610650	A1610650
C 440	15.4	1.4	50	9	AU102380	AU102380	C 513	15.2	1.4	46	9	A1680115	A1680115
C 441	15.4	1.4	50	9	AU102377	AU102377	C 514	15.2	1.4	46	9	AV833431	AV833431
C 442	15.4	1.4	50	9	AU102882	AU102882	C 515	15.2	1.4	46	9	AV833431	AV833431
C 443	15.4	1.4	50	9	AU103025	AU103025	C 516	15.2	1.4	46	12	AZ496495	AZ496495
C 444	15.4	1.4	50	9	AU103025	AU103025	C 517	15.2	1.4	46	12	AZ596992	AZ596992
C 445	15.4	1.4	50	9	AU103025	AU103025	C 518	15.2	1.4	46	12	AZ621438	AZ621438
C 446	15.4	1.4	50	9	AU103025	AU103025	C 519	15.2	1.4	46	12	AZ838956	AZ838956
C 447	15.4	1.4	50	9	AU103025	AU103025	C 520	15.2	1.4	47	10	B1053798	B1053798
C 448	15.4	1.4	50	9	AU103025	AU103025	C 521	15.2	1.4	47	10	TE56338	TE56338
C 449	15.4	1.4	50	9	AU103025	AU103025	C 522	15.2	1.4	47	10	BE732251	BE732251
C 450	15.4	1.4	50	9	AU103025	AU103025	C 523	15.2	1.4	47	12	AZ481505	AZ481505
C 451	15.4	1.4	50	9	AU103025	AU103025	C 524	15.2	1.4	48	12	AAW497611	AAW497611
C 452	15.4	1.4	50	9	AU103025	AU103025	C 525	15.2	1.4	48	12	AZ443721	AZ443721
C 453	15.4	1.4	50	9	AU103025	AU103025	C 526	15.2	1.4	48	12	AZ588342	AZ588342
C 454	15.4	1.4	50	9	AU103025	AU103025	C 527	15.2	1.4	48	12	AZ594565	AZ594565
C 455	15.4	1.4	50	9	AU103025	AU103025	C 528	15.2	1.4	48	12	AZ760053	AZ760053



529	15.2	1.4	48	12	A2785682	A2785682 2M0029M16	602	15	1.4	43	9	AA928331	AA928331 cm76c12.s
C 530	15.2	1.4	48	12	TA360A090	AL495496 T. brucei	C 603	15	1.4	43	9	A1915674	A1915674 w973g01.x
C 531	15.2	1.4	49	9	AA681490	AA681490 vr42a01.s	C 604	15	1.4	43	9	AU009119	AU009119
532	15.2	1.4	49	9	AA889788	AA889788 a151a10.s	C 605	15	1.4	43	10	BM397403	BM397403 5009-0-32
C 533	15.2	1.4	49	9	AA928990	AA928990 o027e03.s	C 606	15	1.4	43	12	A2474035	A2474035 1M0290F18
C 534	15.2	1.4	49	9	AA971164	AA971164 op11e05.s	C 607	15	1.4	43	12	A2592119	A2592119 1M0402F17
C 535	15.2	1.4	49	9	AA993146	AA993146 oc77a10.s	C 608	15	1.4	43	12	A2643360	A2643360 1M0505B21
C 536	15.2	1.4	49	9	A1006832	A1006832 ua74e06.t	C 609	15	1.4	43	12	A2875350	A2875350 2M0189M19
C 537	15.2	1.4	49	9	AA146415	AA146415 wr66c08.t	C 610	15	1.4	43	12	TA44H020	TA44H020
C 538	15.2	1.4	49	9	A1545773	A1545773 fb5BD02.Y	C 611	15	1.4	44	9	A1357277	A1357277 qx15f01.x
539	15.2	1.4	49	9	A1814770	A1814770 wr65e08.x	C 612	15	1.4	44	9	AV833723	AV833723
540	15.2	1.4	49	9	AV860511	AV860511	C 613	15	1.4	44	10	HE4101	HE4101 yr57e01.r1
541	15.2	1.4	49	10	D12159	D12159 HUM0005261	C 614	15	1.4	44	10	779926	779926 y085a06.s1
C 542	15.2	1.4	49	12	A2665591	A2665591 1M0547D09	C 615	15	1.4	45	9	AA276118	AA276118 vc36d12.r
C 543	15.2	1.4	49	12	A2783979	A2783979 2M0026K08	C 616	15	1.4	45	12	A2392238	A2392238 1M0154F09
544	15.2	1.4	49	12	A2971265	A2971265 2M0244N12	C 617	15	1.4	45	12	A2595315	A2595315 1M0407B24
545	15.2	1.4	50	9	AU102241	AU102241	C 618	15	1.4	45	12	A2618901	A2618901 1M0450B22
C 546	15.2	1.4	50	9	AU102281	AU102281	C 621	15	1.4	46	9	AA953796	AA953796 T. brucei
C 547	15.2	1.4	50	9	AU102385	AU102385	C 622	15	1.4	46	9	A1196023	A1196023
C 548	15.2	1.4	50	9	AU102442	AU102442	C 623	15	1.4	46	10	C02279	C02279
C 549	15.2	1.4	50	9	AU102503	AU102503	C 624	15	1.4	46	10	N77017	N77017
C 550	15.2	1.4	50	9	AU102689	AU102689	C 625	15	1.4	46	12	A2486324	A2486324
551	15.2	1.4	50	9	AU102690	AU102690	C 626	15	1.4	46	12	TA339F10P	TA339F10P
C 552	15.2	1.4	50	9	AU102892	AU102892	C 627	15	1.4	47	12	B036254	B036254
C 553	15.2	1.4	50	9	AU102946	AU102946	C 628	15	1.4	47	12	A2403460	A2403460
C 554	15.2	1.4	50	9	AU103388	AU103388	C 629	15	1.4	48	12	A2852673	A2852673 np13d01.s
C 555	15.2	1.4	50	9	AU103758	AU103758	C 630	15	1.4	48	10	220559	220559 HSAACUCU.T
C 556	15.2	1.4	50	9	AU103810	AU103810	C 631	15	1.4	48	10	BE541054	BE541054 601064008
557	15.2	1.4	50	9	AU104965	AU104965	C 632	15	1.4	48	12	A2784814	A2784814 2M0028M02
558	15.2	1.4	50	9	AU105262	AU105262	C 633	15	1.4	48	12	A2816555	A2816555 2M0085B21
559	15.2	1.4	50	9	AU105788	AU105788	C 634	15	1.4	48	12	TA269C12Q	TA269C12Q
560	15.2	1.4	50	9	AU105788	AU105788	C 635	15	1.4	49	9	AA657267	AA657267 vr27d07.r
C 561	15.2	1.4	50	9	AU105802	AU105802	C 636	15	1.4	49	9	AA937999	AA937999 co78d03.s
C 562	15.2	1.4	50	9	AU105909	AU105909	C 637	15	1.4	49	9	AT334100	AT334100
C 563	15.2	1.4	50	9	AU105945	AU105945	C 638	15	1.4	49	9	A1394134	A1394134 qp97c03.x
C 564	15.2	1.4	50	9	AU106737	AU106737	C 639	15	1.4	49	9	A1931109	A1931109 fc77a05.x
C 565	15.2	1.4	50	9	AU107081	AU107081	C 640	15	1.4	49	9	AA199668	AA199668 zq75d01.s
C 566	15.2	1.4	50	9	AA551834	AA551834 0158d08.s	C 641	15	1.4	49	10	BG154468	BG154468 ba50b03.x
567	15.2	1.4	50	12	A2408537	A2408537 1M0179G14	C 642	15	1.4	49	12	A2418466	A2418466 1M0194L05
568	15	1.4	28	12	A2512393	A2512393 1M0357F20	C 643	15	1.4	49	12	A2529327	A2529327 1M0209P11
569	15	1.4	29	12	A2433472	A2433472 1M0219A24	C 644	15	1.4	49	9	AA199668	AA199668 1M0416L11
570	15	1.4	29	12	A2623422	A2623422 1M0464F20	C 645	15	1.4	49	12	A27760264	A27760264 1M0553H20
571	15	1.4	31	9	A2759923	A2759923 1M0553I10	C 646	15	1.4	49	10	BG154468	BG154468 2M0001O10
C 572	15	1.4	31	9	A1003105	A1003105 an27e04.s	C 647	15	1.4	49	12	A2812913	A2812913 2M0079M19
C 573	15	1.4	31	9	A1916434	A1916434 tx07f03.x	C 648	15	1.4	49	12	A2995208	A2995208 2M0280O19
574	15	1.4	31	12	A2500072	A2500072 1M0338A14	C 649	15	1.4	49	9	AU102227	AU102227
575	15	1.4	32	12	A2815018	A2815018 2M0083G02	C 650	15	1.4	50	9	AU102443	AU102443
C 576	15	1.4	33	12	A2455599	A2455599 1M0080P15	C 651	15	1.4	50	9	AU102633	AU102633
577	15	1.4	33	12	A2635722	A2635722 1M0493H24	C 652	15	1.4	50	9	AU102683	AU102683
C 578	15	1.4	34	9	AA907684	AA907684 om11e03.s	C 653	15	1.4	50	9	AU103143	AU103143
C 579	15	1.4	34	9	A1168400	A1168400 ga25e03.s	C 654	15	1.4	50	9	AU103148	AU103148
580	15	1.4	34	9	A1286646	A1286646 ub94G11.r	C 655	15	1.4	50	9	AU104870	AU104870
C 581	15	1.4	34	12	A2419323	A2419323 1M0306K18	C 656	15	1.4	50	9	AU105409	AU105409
582	15	1.4	36	12	A2482026	A2482026	C 657	15	1.4	50	9	AU105414	AU105414
C 583	15	1.4	37	9	A1018376	A1018376 ov41e01.s	C 658	15	1.4	50	9	AU105417	AU105417
C 584	15	1.4	37	10	T52826	T52826 ya81D02.s1	C 659	15	1.4	50	9	AU105761	AU105761
C 585	15	1.4	37	12	A2479159	A2479159 1M0299E10	C 660	15	1.4	50	9	AU105762	AU105762
C 586	15	1.4	38	12	BH023763	BH023763 BG02168-5	C 661	15	1.4	50	9	AU105859	AU105859
587	15	1.4	38	12	A2311889	A2311889 1M0027F06	C 662	15	1.4	50	9	AU106551	AU106551
C 588	15	1.4	39	12	A2992897	A2992897 2M0277P09	C 663	15	1.4	50	9	AU106949	AU106949
C 589	15	1.4	40	9	AA865280	AA865280 cg88H02.s	C 664	15	1.4	50	9	AU107025	AU107025
590	15	1.4	40	9	A1021601	A1021601 ub09f01.r	C 665	15	1.4	50	9	AU107152	AU107152
591	15	1.4	40	12	A2622537	A2622537 1M0459L12	C 666	15	1.4	50	9	AU107700	AU107700
592	15	1.4	40	12	A2772390	A2772390 1M0583C17	C 667	15	1.4	50	9	AU107723	AU107723
593	15	1.4	41	10	D20674	D20674 HUMGSO1650	C 668	15	1.4	50	9	AU108051	AU108051
C 594	15	1.4	41	10	R85401	R85401 yq22a03.s1	C 669	15	1.4	50	9	AM396348	AM396348
C 595	15	1.4	41	12	TA817432	TA817432 2M0086M11	C 670	15	1.4	50	10	BE310235	BE310235
C 596	15	1.4	42	12	TA324E070	TA324E070	C 671	15	1.4	50	12	A2763489	A2763489
C 597	15	1.4	42	12	BE278008	BE278008 601179881	C 672	15	1.4	50	12	AA2763489	AA2763489
C 598	15	1.4	42	12	A2342894	A2342894 1M0076B14	C 673	15	1.4	50	12	AA2763489	AA2763489
C 599	15	1.4	42	12	A2344190	A2344190 1M0078M02	C 674	15	1.4	50	12	AA2763489	AA2763489
600	15	1.4	42	12	A2647857	A2647857 1M0514P04	C 675	15	1.4	50	12	AA2763489	AA2763489
601	15	1.4	42	12	A2647857	A2647857 1M0514P04	C 676	15	1.4	50	12	AA2763489	AA2763489

675	15	1.4	50	12	AZ826565	2M0105D08	748	14.8	1.4	48	12	AZ973732	AZ973732	2M0248M01
676	14.8	1.4	28	12	AZ759516	1M0552C12	C 749	14.8	1.4	49	9	AI036907	AI036907	un21h04.r
677	14.8	1.4	29	12	AZ759510	2M0057B24	C 750	14.8	1.4	49	9	AI493938	AI493938	qz94h01.x
678	14.8	1.4	31	10	BM398905	5009-0-50	C 751	14.8	1.4	49	9	AV833481	AV833481	AV833481
679	14.8	1.4	32	10	BF667712	60212230	C 752	14.8	1.4	49	9	AA428132	AA428132	2819791.5
680	14.8	1.4	32	12	AZ776494	2M0010I07	C 753	14.8	1.4	49	9	AA428326	AA428326	zw18e03.s
681	14.8	1.4	33	10	BG387814	602412712	C 754	14.8	1.4	49	9	AA429584	AA429584	zww77h05.r
682	14.8	1.4	34	9	AA616465	vm66d01.r	C 755	14.8	1.4	49	10	BM307546	BM307546	sak30f06.
683	14.8	1.4	34	10	B0067168	B0067168	C 756	14.8	1.4	49	10	H97554	H97554	ym04h01.s1
684	14.8	1.4	34	12	AZ795396	2M0049A11	C 757	14.8	1.4	49	10	N93241	N93241	zbb6b07.s1
685	14.8	1.4	35	12	AZ481652	1M0306I05	C 758	14.8	1.4	49	10	BF506858	BF506858	10005P-22
686	14.8	1.4	35	12	AZ498988	1M0337022	C 759	14.8	1.4	49	12	AZ578707	AZ578707	26c12.Sho
687	14.8	1.4	36	10	BJ077335	BJ077335	C 760	14.8	1.4	49	12	AZ770123	AZ770123	1M0571D03
688	14.8	1.4	36	12	AZ345585	1M0080M16	C 761	14.8	1.4	49	12	AZ804582	AZ804582	2M0065009
689	14.8	1.4	36	12	AZ785181	2M0028I20	C 762	14.8	1.4	49	12	AI252059	AI252059	qv39f04.x
690	14.8	1.4	36	12	AZ837283	2M0132B05	C 763	14.8	1.4	49	9	AI023133	AI023133	AI023133
691	14.8	1.4	37	9	AA983487	or45h03.s	C 764	14.8	1.4	49	9	AI023314	AI023314	AI023314
692	14.8	1.4	37	9	AI051308	ox24d05.x	C 765	14.8	1.4	49	9	AI023315	AI023315	AI023315
693	14.8	1.4	37	9	AI197047	ue50g11.r	C 766	14.8	1.4	49	9	AI023315	AI023315	AI023315
694	14.8	1.4	37	9	AI384339	fb07h03.y	C 767	14.8	1.4	49	9	AI023315	AI023315	AI023315
695	14.8	1.4	37	9	AI632588	AL632588	C 768	14.8	1.4	49	9	AI023315	AI023315	AI023315
696	14.8	1.4	37	9	AA154541	mq68g03.r	C 769	14.8	1.4	49	9	AI023315	AI023315	AI023315
697	14.8	1.4	37	12	TA130F10P	AL64415.T. bruce1	C 770	14.8	1.4	49	9	AI023315	AI023315	AI023315
698	14.8	1.4	37	12	TA234G07Q	AL481264.T. bruce1	C 771	14.8	1.4	49	9	AI023315	AI023315	AI023315
699	14.8	1.4	38	12	AA796605	vp31e06.r	C 772	14.8	1.4	49	9	AI023315	AI023315	AI023315
700	14.8	1.4	38	12	AZ834173	2M0116D14	C 773	14.8	1.4	49	9	AI023315	AI023315	AI023315
701	14.8	1.4	39	12	BG106628	602290452	C 774	14.8	1.4	49	9	AI023315	AI023315	AI023315
702	14.8	1.4	39	12	AZ428899	1M0201H13	C 775	14.8	1.4	49	9	AI023315	AI023315	AI023315
703	14.8	1.4	40	9	AA035761	zk28f07.r	C 776	14.8	1.4	49	9	AI023315	AI023315	AI023315
704	14.8	1.4	40	9	AI047550	uh80b09.r	C 777	14.8	1.4	49	9	AI023315	AI023315	AI023315
705	14.8	1.4	40	9	AI118960	ue23b06.x	C 778	14.8	1.4	49	9	AI023315	AI023315	AI023315
706	14.8	1.4	40	9	AI362416	qv92e11.x	C 779	14.8	1.4	49	9	AI023315	AI023315	AI023315
707	14.8	1.4	40	10	D44765	HUMSUPY95	C 780	14.8	1.4	49	9	AI023315	AI023315	AI023315
708	14.8	1.4	43	9	AA721327	n259d12.s	C 781	14.8	1.4	49	9	AI023315	AI023315	AI023315
709	14.8	1.4	43	9	AA911375	od90g01.s	C 782	14.8	1.4	49	9	AI023315	AI023315	AI023315
710	14.8	1.4	43	9	AA976713	oq06d06.s	C 783	14.8	1.4	49	9	AI023315	AI023315	AI023315
711	14.8	1.4	43	9	AI283683	qj72g11.x	C 784	14.8	1.4	49	9	AI023315	AI023315	AI023315
712	14.8	1.4	43	9	AI351416	qg37h01.x	C 785	14.8	1.4	49	9	AI023315	AI023315	AI023315
713	14.8	1.4	43	9	AA197516	mu18d04.r	C 786	14.8	1.4	49	9	AI023315	AI023315	AI023315
714	14.8	1.4	43	9	AA227334	zr17h11.r	C 787	14.8	1.4	49	9	AI023315	AI023315	AI023315
715	14.8	1.4	43	10	W62611	md56c07.r1	C 788	14.8	1.4	49	9	AI023315	AI023315	AI023315
716	14.8	1.4	43	12	AZ345681	1M0082G01	C 789	14.8	1.4	49	9	AI023315	AI023315	AI023315
717	14.8	1.4	43	12	AZ771147	1M0573B07	C 790	14.8	1.4	49	9	AI023315	AI023315	AI023315
718	14.8	1.4	43	12	AZ787408	2M0033A05	C 791	14.8	1.4	49	9	AI023315	AI023315	AI023315
719	14.8	1.4	44	12	BE738321	601572701	C 792	14.8	1.4	49	9	AI023315	AI023315	AI023315
720	14.8	1.4	44	12	AZ389567	1M0150E19	C 793	14.8	1.4	49	9	AI023315	AI023315	AI023315
721	14.8	1.4	45	9	AA848952	AV848952	C 794	14.8	1.4	49	9	AI023315	AI023315	AI023315
722	14.8	1.4	45	10	BG111883	602283496	C 795	14.8	1.4	49	9	AI023315	AI023315	AI023315
723	14.8	1.4	45	10	B0034679	BU034679	C 796	14.8	1.4	49	9	AI023315	AI023315	AI023315
724	14.8	1.4	45	12	AZ391553	1M0153D14	C 797	14.8	1.4	49	9	AI023315	AI023315	AI023315
725	14.8	1.4	45	12	AZ445734	1M0241M16	C 798	14.8	1.4	49	9	AI023315	AI023315	AI023315
726	14.8	1.4	45	12	AZ507560	1M0349E13	C 799	14.8	1.4	49	9	AI023315	AI023315	AI023315
727	14.8	1.4	45	12	AZ805160	2M0068I02	C 800	14.8	1.4	49	9	AI023315	AI023315	AI023315
728	14.8	1.4	45	12	AZ809438	2M0073M23	C 801	14.8	1.4	49	9	AI023315	AI023315	AI023315
729	14.8	1.4	46	9	AA869478	vm66d01.r	C 802	14.8	1.4	49	9	AI023315	AI023315	AI023315
730	14.8	1.4	46	9	AI078156	oz30c07.x	C 803	14.8	1.4	49	9	AI023315	AI023315	AI023315
731	14.8	1.4	46	9	AI1218690	ck39a02.x	C 804	14.8	1.4	49	9	AI023315	AI023315	AI023315
732	14.8	1.4	46	9	AI470670	tj13d03.x	C 805	14.8	1.4	49	9	AI023315	AI023315	AI023315
733	14.8	1.4	46	9	AI809473	wh76c10.x	C 806	14.8	1.4	49	9	AI023315	AI023315	AI023315
734	14.8	1.4	46	9	AI811483	tw45d02.x	C 807	14.8	1.4	49	9	AI023315	AI023315	AI023315
735	14.8	1.4	46	9	AI937716	wp83d02.x	C 808	14.8	1.4	49	9	AI023315	AI023315	AI023315
736	14.8	1.4	46	9	AV834346	AV834346	C 809	14.8	1.4	49	9	AI023315	AI023315	AI023315
737	14.8	1.4	46	10	BI756730	603024581	C 810	14.8	1.4	49	9	AI023315	AI023315	AI023315
738	14.8	1.4	46	10	RA8775	y169c01.s1	C 811	14.8	1.4	49	9	AI023315	AI023315	AI023315
739	14.8	1.4	46	10	W75419	me50b03.r1	C 812	14.8	1.4	49	9	AI023315	AI023315	AI023315
740	14.8	1.4	46	12	AZ440102	1M0231F06	C 813	14.8	1.4	49	9	AI023315	AI023315	AI023315
741	14.8	1.4	47	9	AV833944	AV833944	C 814	14.8	1.4	49	9	AI023315	AI023315	AI023315
742	14.8	1.4	47	12	AZ765062	1M0561K15	C 815	14.8	1.4	49	9	AI023315	AI023315	AI023315
743	14.8	1.4	48	9	AI384185	fb17f03.y	C 816	14.8	1.4	49	9	AI023315	AI023315	AI023315
744	14.8	1.4	48	9	AA832607	AV832607	C 817	14.8	1.4	49	9	AI023315	AI023315	AI023315
745	14.8	1.4	48	12	AA025151	EP(3)1015	C 818	14.8	1.4	49	9	AI023315	AI023315	AI023315
746	14.8	1.4	48	12	AZ312539	1M0028E20	C 819	14.8	1.4	49	9	AI023315	AI023315	AI023315
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C 824	14.6	1.3	25	12	A2307448	A2307448	1M0009B03	C 897	14.6	1.3	44	12	A2968547	A2968547	2M0240J23
C 825	14.6	1.3	26	12	A2657444	A2657444	1M0053A15	C 898	14.6	1.3	45	10	AU006728	AU006728	AU006728
C 826	14.6	1.3	27	12	A2430561	A2430561	1M0215P02	C 899	14.6	1.3	45	10	BJ033065	BJ033065	BJ033065
C 827	14.6	1.3	30	10	BE728181	BE728181	601563A91	C 900	14.6	1.3	45	12	A2331000	A2331000	1M0036F24
C 828	14.6	1.3	30	12	A2642986	A2642986	1M0506F16	C 901	14.6	1.3	45	12	A2791420	A2791420	2M0041O14
C 829	14.6	1.3	30	12	A2666770	A2666770	1M0549G08	C 902	14.6	1.3	45	12	A2804529	A2804529	2M0065E02
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C 836	14.6	1.3	33	12	A2359461	A2359461	1M0102K16	C 909	14.6	1.3	46	9	AA180108	AA180108	zp34h01.X
C 837	14.6	1.3	33	12	A2805273	A2805273	2M0066O04	C 910	14.6	1.3	46	9	AL662555	AL662555	AL662555
C 838	14.6	1.3	33	12	TA281G02P	TA281G02P	1M0376P20	C 911	14.6	1.3	46	9	AA244715	AA244715	mx31f12.T
C 839	14.6	1.3	34	9	A1788546	A1788546	uK46d01.X	C 912	14.6	1.3	46	10	W91341	W91341	mg17d01.T
C 840	14.6	1.3	35	12	A2486905	A2486905	1M0316N09	C 913	14.6	1.3	46	12	A2473391	A2473391	1M0225E09
C 841	14.6	1.3	35	12	BF159227	BF159227	601766662	C 914	14.6	1.3	46	12	A2642240	A2642240	1M0505K10
C 842	14.6	1.3	36	12	A2309288	A2309288	1M0013L19	C 915	14.6	1.3	47	9	AVB32665	AVB32665	AVB32665
C 843	14.6	1.3	36	12	A2320138	A2320138	1M0040I06	C 916	14.6	1.3	47	12	A2460642	A2460642	1M0266M03
C 844	14.6	1.3	36	12	A2452052	A2452052	1M0251O10	C 917	14.6	1.3	47	12	A2787487	A2787487	2M0033J07
C 845	14.6	1.3	36	12	A2787755	A2787755	2M0034I23	C 918	14.6	1.3	47	12	TA262B06P	TA262B06P	TA262B06P
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C 848	14.6	1.3	37	9	A1634572	A1634572	tz30a01.X	C 921	14.6	1.3	48	10	D12328	D12328	H0M0008B04
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C 852	14.6	1.3	37	12	A2782132	A2782132	2M0022D08	C 925	14.6	1.3	48	12	A2514491	A2514491	1M0361G22
C 853	14.6	1.3	37	12	A2810046	A2810046	2M0074C23	C 926	14.6	1.3	48	12	A2831243	A2831243	2M0110F20
C 854	14.6	1.3	38	10	AV834048	AV834048	AV834048	C 927	14.6	1.3	49	9	AA013617	AA013617	mh10d05.X
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C 858	14.6	1.3	39	12	A2387174	A2387174	1M0146J19	C 931	14.6	1.3	49	9	AA983890	AA983890	af09d11.S
C 859	14.6	1.3	39	12	A2464330	A2464330	1M0273H11	C 932	14.6	1.3	49	9	A1186519	A1186519	0P63d04.S
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C 861	14.6	1.3	40	9	AA962768	AA962768	0O90D07.S	C 934	14.6	1.3	49	9	A1109988	A1109988	ml6e02.X
C 862	14.6	1.3	40	9	AA164815	AA164815	z099g09.S	C 935	14.6	1.3	49	9	A1736565	A1736565	sb30e08.Y
C 863	14.6	1.3	40	9	AA631276	AA631276	ng92c01.S	C 936	14.6	1.3	49	9	A1951873	A1951873	w38607.X
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C 865	14.6	1.3	40	12	A2772872	A2772872	1M0584C05	C 938	14.6	1.3	49	9	AA101472	AA101472	1M01472
C 866	14.6	1.3	40	12	A2784448	A2784448	2M0027E04	C 939	14.6	1.3	49	10	BG545925	BG545925	602573219
C 867	14.6	1.3	40	12	A2793917	A2793917	2M0047L24	C 940	14.6	1.3	49	10	BJ054665	BJ054665	BJ054665
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C 870	14.6	1.3	41	9	A1167547	A1167547	0X67h12.S	C 943	14.6	1.3	49	12	BE019201	BE019201	uY02d01.Y
C 871	14.6	1.3	41	10	BF1830856	BF1830856	603080973	C 944	14.6	1.3	49	12	A2500888	A2500888	1M0339C03
C 872	14.6	1.3	41	10	BF1836557	BF1836557	603080950	C 945	14.6	1.3	49	12	A2511220	A2511220	1M0336I08
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C 875	14.6	1.3	41	12	TA586D04P	TA586D04P	1M0581390	C 948	14.6	1.3	49	12	AA114391	AA114391	MBAFCE4A0
C 876	14.6	1.3	42	10	BE395464	BE395464	601309989	C 949	14.6	1.3	50	9	AA210000	AA210000	mu39c03.X
C 877	14.6	1.3	42	10	A2377659	A2377659	1M0132C07	C 950	14.6	1.3	50	9	AA634703	AA634703	AL634703
C 878	14.6	1.3	42	12	A2650453	A2650453	1M0520F10	C 951	14.6	1.3	50	9	AU013922	AU013922	1M013922
C 879	14.6	1.3	42	12	AA908443	AA908443	0G81a03.S	C 952	14.6	1.3	50	9	AU0102393	AU0102393	1M0102393
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C 886	14.6	1.3	43	9	AA194879	AA194879	u157H07.X	C 959	14.6	1.3	50	9	AU0103457	AU0103457	1M0103457
C 887	14.6	1.3	43	9	AA194879	AA194879	u157H07.X	C 960	14.6	1.3	50	9	AU0103464	AU0103464	1M0103464
C 888	14.6	1.3	43	10	TA5717	TA5717	Yc16f09.r1	C 961	14.6	1.3	50	9	AU0103465	AU0103465	1M0103465
C 889	14.6	1.3	43	12	AA776656	AA776656	2M0010B04	C 962	14.6	1.3	50	9	AU0103466	AU0103466	1M0103466
C 890	14.6	1.3	44	10	AA776656	AA776656	2M0010B04	C 963	14.6	1.3	50	9	AU0103467	AU0103467	1M0103467
C 891	14.6	1.3	44	10	AA776656	AA776656	2M0010B04	C 964	14.6	1.3	50	9	AU0103468	AU0103468	1M0103468
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C 893	14.6	1.3	44	12	AA441185	AA441185	1M0232C01	C 966	14.6	1.3	50	9	AU0104537	AU0104537	1M0104537
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## ALIGNMENTS

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VERSION AUI06328.1 GI:13555849
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
JOURNAL Contact: Yutaka Suzuki
MEDLINE Department of Virology
COMMENT Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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1 CCGTACGTCCGCTTACGAGCTGGCGCAGACATGCTGGCGGATGAGGC 49

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DEFINITION AUI06270 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION AUI06270
VERSION AUI06270
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
JOURNAL Contact: Yutaka Suzuki
MEDLINE Department of Virology
COMMENT Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
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IMAGE:1382096 3' similar to SW:AT1_PAT P55009 ALLOGRAFT
INFLAMMATORY FACTOR-1; mRNA sequence.
ACCESSION AA960633
VERSION AA960633.1 GI:3126533
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 46)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

```

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.  
The WashU-HMI Mouse EST Project  
Unpublished (1996)  
Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:904564  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers

# FEATURES

1. .46  
Location/Qualifiers

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/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia) digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."  
BASE COUNT 13 a 12 c 8 g 13 t  
ORIGIN

Query Match 1.7%; Score 19; DB 9; Length 46;  
Best Local Similarity 65.1%; Pred. No. 4.7e+05;  
Matches 28; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 181 ATTATATCTTGGAAGACTTGAGATACCTTGCCATCAAA 223  
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RESULT 4  
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DEFINITION clone IMAGE:1679350 3' similar to TR:014296 Q14296 FAST KINASE. ;  
VERSION AI074316  
KEYWORDS EST.  
SOURCE AI074316.1 GI:3400960  
ORGANISM human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 49)  
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
Tumor Gene Index  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Unpublished (1997)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgapbs-remail.nih.gov

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 2264 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 1.  
Location/Qualifiers  
1. .49  
Location/Qualifiers

Source  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1679350"  
/clone\_lib="Soares-senescent\_fibroblasts\_NBHSF"  
/tissue\_type="senescent fibroblast"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Vector: pT73D (Pharmacia) with a modified polylinker V-TYPE: phagemid; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5].  
TCTTACCATCTGGAAGTGGAGCGCCCATTTTCTTTTCTTTT 3',  
double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo."  
BASE COUNT 14 a 15 c 12 g 8 t  
ORIGIN

Query Match 1.7%; Score 19; DB 9; Length 49;  
Best Local Similarity 71.4%; Pred. No. 4.9e+05;  
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 373 CACAGTGTGATGCTGTGAGCGACCAATTTATGCT 407  
Db 45 CTCAGAGTTCGTGCTGAGCGCCACACATTCGGGT 11

RESULT 5  
AU105328/c 50 bp mRNA linear EST 30-AUG-2001  
LOCUS AU105328 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
DEFINITION HRC00662, mRNA sequence.  
ACCESSION AU105328  
VERSION AU105328.1 GI:13554849  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 50)  
Suzuki, Y., Talira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, Y., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)  
MEDLINE 21270072  
COMMENT Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokane-dai, Minatoku, Tokyo 108-8639, Japan  
Email: yusuzuki@ims.u-tokyo.ac.jp  
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S.  
Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES  
1. .50  
Location/Qualifiers

Source  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="HRC00662"  
/clone\_lib="Sugano Homo sapiens cDNA library"  
BASE COUNT 10 a 12 c 13 g 15 t  
ORIGIN

Query Match 1.7%; Score 19; DB 9; Length 50;  
Best Local Similarity 65.1%; Pred. No. 5e+05;  
Matches 28; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 531 CTTACTGAACCATCTGCTTGACCGATTGAGTCAGGCCA 573  
 Db 43 CTGAACGCAATCTCGCTTGCTGCGATTAATCTGAGCGCA 1

## RESULT 6

LOCUS AU106825/c 50 bp mRNA linear EST 30-AUG-2001  
 DEFINITION AU106825 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
 CAS01421, mRNA sequence.  
 ACCESSION AU106825  
 VERSION AU106825.1 GI:13556346  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

## REFERENCE

AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata  
 'H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki  
 'Y., Nakamura, Y., Suyama, A. and Sugano, S.  
 Diverse transcriptional initiation revealed by fine, large-scale  
 mapping of mRNA start sites  
 EMBO Rep. 2 (5), 388-393 (2001)

## COMMENT

JOURNAL MEDLINE  
 TITLE Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yusuzuki@ims.u-tokyo.ac.jp  
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano  
 'S. Construction and characterization of a full length-enriched and  
 a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).  
 Location/Qualifiers  
 1..50  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="CAS01421"  
 /clone\_lib="Sugano Homo sapiens cDNA library"  
 12 a 10 c 19 g 9 t

## FEATURES

BASE COUNT  
 ORIGIN  
 Query Match 1.7%; Score 19; DB 9; Length 50;  
 Best Local Similarity 65.1%; Pred. No. 5e+05;  
 Matches 28; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 296 ATGATCTGGCCAGCCATCTTGTCTCCTCAACAGTATGTCAT 338  
 50 ATGCCCGACCGCCAGCGCTCTCTCCGAACGAGCTGACAT 8

RESULT 7  
 LOCUS H39422/c 45 bp mRNA linear EST 27-AUG-1996  
 DEFINITION DR116 IFNgamma-induced astrocyte ESTs Rattus norvegicus cDNA clone  
 DR116 5'-end with RP similar to unknown sequence, mRNA sequence.  
 ACCESSION H39422  
 VERSION H39422.1 GI:915097  
 KEYWORDS EST.  
 SOURCE Norway rat.  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

REFERENCE 1 (bases 1 to 45)  
 Kuchinke, W., Hart, R.P. and Jonakait, G.M.  
 Identification of mRNAs regulated by interferon-gamma in cultured  
 rat astrocytes by PCR differential display  
 Neuroimmunomodulation 2, 347-355 (1995)

JOURNAL MEDLINE  
 TITLE Contact: Hart RP  
 Rutgers University  
 Dept of Biol Sci, Rutgers University, 101 Warren St, Newark NJ

BASE COUNT  
 ORIGIN  
 12 a 11 c 8 g 14 t

07102  
 Tel: 2016481008  
 Fax: 2016481007  
 Email: thart@andromeda.rutgers.edu  
 unknown sequence  
 direct sequencing  
 Seq primer: AGGTGACCGT.  
 Location/Qualifiers  
 1..45  
 /organism="Rattus norvegicus"  
 /strain="Sprague-Dawley"  
 /db\_xref="taxon:10116"  
 /clone="DR116"  
 /clone\_lib="IFNgamma-induced astrocyte ESTs"  
 /note="cDNA from IFNgamma-induced cultured rat astrocytes  
 was screened by PCR differential display. Regulated cDNAs  
 were amplified, sequenced and confirmed by dot-blot and  
 Northern."

## FEATURES

BASE COUNT  
 ORIGIN  
 Query Match 1.7%; Score 18.8; DB 10; Length 45;  
 Best Local Similarity 68.4%; Pred. No. 5.3e+05;  
 Matches 26; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 271 GCTCTAGCAGGACGATCTTGCGATGATCTGAGGCCA 308  
 Db 45 GCTCTAGCAGCAGCAGCCCTAAAGCTGATGATCTTCA 8

RESULT 8  
 LOCUS H39423/c 45 bp mRNA linear EST 27-AUG-1996  
 DEFINITION DR117 IFNgamma-induced astrocyte ESTs Rattus norvegicus cDNA clone  
 DR117 5'-end with RP similar to unknown sequence, mRNA sequence.  
 ACCESSION H39423  
 VERSION H39423.1 GI:915098  
 KEYWORDS EST.  
 SOURCE Norway rat.  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

REFERENCE 1 (bases 1 to 45)  
 Kuchinke, W., Hart, R.P. and Jonakait, G.M.  
 Identification of mRNAs regulated by interferon-gamma in cultured  
 rat astrocytes by PCR differential display  
 Neuroimmunomodulation 2, 347-355 (1995)

JOURNAL MEDLINE  
 TITLE Contact: Hart RP  
 Rutgers University  
 Dept of Biol Sci, Rutgers University, 101 Warren St, Newark NJ  
 07102  
 Tel: 2016481008  
 Fax: 2016481007  
 Email: thart@andromeda.rutgers.edu  
 unknown sequence  
 direct sequencing  
 Seq primer: AGGTGACCGT.  
 Location/Qualifiers  
 1..45  
 /organism="Rattus norvegicus"  
 /strain="Sprague-Dawley"  
 /db\_xref="taxon:10116"  
 /clone="DR117"  
 /clone\_lib="IFNgamma-induced astrocyte ESTs"  
 /note="cDNA from IFNgamma-induced cultured rat astrocytes  
 was screened by PCR differential display. Regulated cDNAs  
 were amplified, sequenced and confirmed by dot-blot and  
 Northern."

BASE COUNT  
 ORIGIN  
 12 a 11 c 8 g 14 t

```

JOURNAL      Mapping of mRNA start sites
MEDLINE     EMBO Rep. 2 (5), 388-393 (2001)
COMMENT     21270072
            Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: yusuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,
            S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
SOURCE
    location/Qualifiers
        1..50
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone="HS106872"
        /clone_1lb="Sugano Homo sapiens cDNA Library"
BASE COUNT   10 a       18 c       10 g       12 t
ORIGIN
Query Match          1.7%, Score 18.6; DB 9; Length 50;
Best Local Similarity 65.9%; Pred. No. 6.5e+05;
Matches 27; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 776 AGAGCGCAAGATTGGACAGAGTTCTTCGATTTGCCTCAT 816
    ||||| | ||||||| ||| |||||||
Db 41 AGGAGCCTCATTTGTGACAGAGTCCACTGACAGAGTCTCAT 1

RESULT 11
LOCUS      A1080507              40 bp      mRNA      linear      EST 12-Aug-1998
DEFINITION o238f11.s1 Soares.NHHMPU.S1 Homo sapiens cDNA clone IMAGE:1677645
           3' similar to RF:O00409 O00409 CHECKPOINT SUPPRESSOR 1 : wpu

```

ACCESSION	AT080507
VERSION	AT080507.1
KEYWORDS	GI:3416758
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eulhelia; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 40)
TITLE	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgaps-ft@mail.nih.gov">cgaps-ft@mail.nih.gov</a> This clone is available royalty-free through LNC <sub>+</sub> ; contact the IMAGE Consortium ( <a href="mailto:info@image.llnl.gov">info@image.llnl.gov</a> ) for further information. Trace considered overall poor quality Seq primer: -40ml3 fwd. ET from Amer sham High quality sequence stop: 1. Location/Qualifiers
FEATURES	1..40
Source	/organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:1677645" /clone_lib="Soares_NhHMPu_S1" /tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus" /lab_host="DH10B" /note="Organ: mixed (see below); Vector: pMT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NBHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 260232-265223, .





DEFINITION *Oryza sativa* DNA, 3' flanking sequence of Tos17 insertion, clone:ND2040\_0\_703\_1A, genomic survey sequence.

ACCESSION AG023852

VERSION AG023852.1 GI:7682027

KEYWORDS GSS: GSS (genome survey sequence).

SOURCE *Oryza sativa* (sub-species: japonica, strain:ND2040, cultivar:Mipponbare) DNA, clone.lib:PCR product directly amplified from rice genomic DNA clone:ND2040\_0\_703\_1A.

ORGANISM *Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.*

REFERENCE 1 (sites)

AUTHORS Miyao, A. and Hirochika, H.

TITLE Rice insertion mutants

JOURNAL Unpublished (1999)

REFERENCE 2 (bases 1 to 47)

AUTHORS Miyao, A., Tanaka, K. and Hirochika, H.

TITLE Direct Submission

JOURNAL Submitted (25-OCT-1999) to the DDBJ/EMBL/Genbank databases. Akio Miyao, National Institute of Agrobiological Resources, Molecular Genetics: 2-1-2, Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:miyao@affrc.go.jp, URL: <http://www.abr.affrc.go.jp/>, Tel:81-298-38-7006, Fax:81-298-38-7006)

FEATURES

source

1. .47

/organism="Oryza sativa"

/cultivar="Mipponbare"

/strain="ND2040"

/sub-species="japonica"

/db\_xref="taxon:4530"

/clone="ND2040\_0\_703\_1A"

/clone.lib="PCR product directly amplified from rice genomic DNA"

/note="Sequence group name: ND2040\_0\_703\_1A. -The 3' end of retrotransposon Tos17 was found immediately upstream of this sequence."

BASE COUNT 14 a 11 c 11 g 8 t 3 others

ORIGIN

Query Match 1.7%; Score 18.2; DB 12; Length 47;

Best Local Similarity 71.9%; Pred. No. 8.1e+05;

Matches 23; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 732 GCTAGCTACTGAGCAGCATGTTGGCAATG 763

1 ||||| 1 || 1 |||||

DB 45 GTTACTACTNCCGTCGCGCATGTCGCAATG 14

RESULT 15

AG025099 48 bp DNA linear GSS 02-MAY-2000

LOCUS AG025099

DEFINITION *Oryza sativa* DNA, 3' flanking sequence of Tos17 insertion, clone:TS133T, genomic survey sequence.

ACCESSION AG025099

VERSION AG025099.1 GI:7683763

KEYWORDS GSS: GSS (genome survey sequence).

SOURCE *Oryza sativa* (sub-species: japonica, strain:NC2532, cultivar:Mipponbare) DNA, clone.lib:PCR product directly amplified from rice genomic DNA clone:TS133T.

ORGANISM *Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.*

REFERENCE 1 (sites)

AUTHORS Miyao, A. and Hirochika, H.

TITLE Rice insertion mutants

JOURNAL Unpublished (1999)

REFERENCE 2 (bases 1 to 48)

AUTHORS Miyao, A., Miyazaki, A., Yamashita, Y. and Hirochika, H.

TITLE Direct Submission

JOURNAL Submitted (25-OCT-1999) to the DDBJ/EMBL/Genbank databases. Akio Miyao, National Institute of Agrobiological Resources, Molecular

Genetics: 2-1-2, Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:miyao@affrc.go.jp, URL: <http://www.abr.affrc.go.jp/>, Tel:81-298-38-7006, Fax:81-298-38-7006)

FEATURES

source

1. .48

/organism="Oryza sativa"

/cultivar="Mipponbare"

/strain="NC2532"

/sub-species="japonica"

/db\_xref="taxon:4530"

/clone="TS133T"

/clone.lib="PCR product directly amplified from rice genomic DNA"

/note="Sequence group name: TS133T. -The 3' end of retrotransposon Tos17 was found immediately upstream of this sequence."

BASE COUNT 16 a 9 c 11 g 12 t

ORIGIN

Query Match 1.7%; Score 18.2; DB 12; Length 48;

Best Local Similarity 66.7%; Pred. No. 8.2e+05;

Matches 26; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 715 AAGAAATCAGCTGCCAGCTAGCTAGCGAGCAGCATGTT 753

1 |||| 1 || 1 |||| 1 |||||

DB 2 ATGATATGAGGTGTGAAGTTGCCACCGAAGACATGCT 40

RESULT 16

AU105082 50 bp mRNA linear EST 30-AUG-2001

LOCUS AU105082

DEFINITION *Sugano Homo sapiens cDNA library Homo sapiens cDNA clone KAT10414, mRNA sequence.*

ACCESSION AU105082

VERSION AU105082.1 GI:13554603

KEYWORDS EST.

SOURCE human.

ORGANISM *Homo sapiens*

REFERENCE 1 (bases 1 to 50)

AUTHORS Mamalia; Eutheria; Primates; Catarhinii; Homiidae; Homo.

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)

MEDLINE 21270072

COMMENT Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshimoto-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S.

FEATURES

source

1. .50

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="KAT10414"

/clone.lib="Sugano Homo sapiens cDNA library"

BASE COUNT 8 a 13 c 18 g 11 t

ORIGIN

Query Match 1.7%; Score 18.2; DB 9; Length 50;

Best Local Similarity 61.7%; Pred. No. 8.4e+05;

Matches 29; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 830 CTGCGTGTGTGGAGAGCGCGTGAGCTTCCCGCTGCACTGTC 876

1 |||| 1 || 1 ||||| 1 |||| 1 ||||

DB 1 CTGAGTGTATGATGTGTGACAGCGTGACCGCATCTGGCCCTGC 47

RESULT 17  
 A1747305 40 bp mRNA linear EST 22-JUN-1999  
 LOCUS u114g09.x1 Sugano mouse embryo mewa Mus musculus cDNA clone  
 DEFINITION IMAGE:2076832.3' similar to TR:018967.018967 HYPOTHETICAL.12.8 KD  
 PROTEIN : mRNA sequence.

ACCESSION A1747305 GI:5125569  
 VERSION A1747305.1  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota: Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 40)  
 Authors: Mairra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, R., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Rittler, E., Kohn, S., Shih, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.  
 The WashU-NCI Mouse EST Project 1999  
 Unpublished (1999)  
 Contact: Mairra M/WashU-NCI Mouse EST Project 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LNL: contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:995268  
 Trace considered overall poor quality  
 Possible reversed clone: similarity on wrong strand  
 Seq primer: custom primer used  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1..40  
 /organism="Mus musculus"  
 /strain="C57BL"  
 /db\_xref="taxon:10090"  
 /clone\_image="2076832"  
 /clone\_lib="Sugano mouse embryo mewa"  
 /dev\_stage="embryo, 14 dpc"  
 /lab\_host="DH10B"  
 /note="Vector: pME18S-FL3; site 1: DraIII (CACTGCTG); site 2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCCTTTTCTTTTCTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCCTACTG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGCTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCTGCTCTTAAAGCTGCG and 3' end primer CGACCTGCACCTCGACACA."

BASE COUNT 3 a 15 c 11 g 11 t  
 ORIGIN

Query Match 1.7%; Score 18; DB 9; Length 40;  
 Best Local Similarity 70.6%; Pred. No. 8.4e+05;  
 Matches 24; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 246 GCCCTTAGGAACCGCTGCGCTCTTGTCTAGCA 279  
 Db 6 GCCTCAGACCCCGCTGCTGTCTCTGCA 39

RESULT 18  
 R81667/c 40 bp mRNA linear EST 12-JUN-1995  
 LOCUS R81667 y102g06.s1 Soares placenta Nb2HP Homo sapiens cDNA clone  
 DEFINITION

IMAGE:147610.3' similar to gb:V00493\_rna1 HEMOGLOBIN ALPHA CHAIN (HUMAN); mRNA sequence.  
 R81667.1 GI:858270  
 EST.

ACCESSION R81667.1 GI:858270  
 VERSION R81667.1  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota: Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 40)  
 Authors: Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Mairra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P., and Wilson, R.  
 The WashU-Merck EST Project  
 Unpublished (1995)  
 Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 Insert Size: 1147  
 High quality sequence starts: 1  
 High quality sequence stops: 1  
 Source: IMAGE Consortium, LNL  
 This clone is available royalty-free through LNL: contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Trace considered overall poor quality  
 Insert Length: 1147 Std Error: 0.00  
 Seq primer: Promega -21m13  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1..40  
 /organism="Homo sapiens"  
 /db\_xref="GDB:558282"  
 /db\_xref="taxon:9606"  
 /clone\_image="147610"  
 /clone\_lib="Soares placenta Nb2HP"  
 /sex="Female"  
 /dev\_stage="placenta obtained at birth (full term)"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /note="Organ: placenta; Vector: pTZ19 (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' AACTGGAATTCGCGCGCCGACGAGATTTTCTTTTCTTTT 3'), double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTZ19 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaiuto."

BASE COUNT 12 a 9 c 10 g 7 t  
 ORIGIN

Query Match 1.7%; Score 18; DB 10; Length 40;  
 Best Local Similarity 77.8%; Pred. No. 8.4e+05;  
 Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 627 TGCATGTCCTTCCAGGTTTGGAT 653  
 Db 38 TGCCTGCGCCCTNCTGCTTGTGAAT 12

RESULT 19  
 AV833081 45 bp mRNA linear EST 22-JUN-2001  
 LOCUS AV833081 K. Sato unpublished cDNA library: Hordeum vulgare subsp. vulgare shoucs germination Hordeum vulgare subsp. vulgare cDNA clone bags11105, mRNA sequence.  
 DEFINITION

ACCESSION AV833081 GI:14525170  
 VERSION AV833081.1  
 KEYWORDS EST  
 SOURCE Hordeum vulgare subsp. vulgare.

## ORGANISM

Hordeum vulgare subsp. vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae  
; Triticeae; Hordeum.  
1 (bases 1 to 45)

## REFERENCE

Barley EST sequencing project in NIG and Okayama Univ

Sato, K.

## AUTHORS

Barley EST sequencing project in NIG and Okayama Univ  
Unpublished (2001)  
Contact: Kazuhiro Sato

## JOURNAL

Research Institute for Bioreresources

Okayama University, Barley Germplasm Center  
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan  
Email: kazsato@rib.okayama-u.ac.jp,  
URL: http://www.rib.okayama-u.ac.jp/barley/  
Sato, K.; Saito, D.; Takeda, K.; Shini, T. and Kohara, Y. Direct  
submission;  
database: http://www.shigen.nig.ac.jp/barley/Barley.html.

## FEATURES

Location/Qualifiers

1..45  
/organism="Hordeum vulgare subsp. vulgare"  
/cultivar="Haruna Nijo"  
/db\_xref="taxon:112509"  
/clone="bags1105"  
/clone\_lib="K. Sato unpublished cDNA library: Hordeum  
vulgare subsp. vulgare shoots germination"  
/tissue\_type="shoots"  
/dev\_stage="germination"  
BASE COUNT 11 a 3 c 19 g 12 t  
ORIGIN

## Query Match

Best Local Similarity 1.7%; Score 18; DB 9; Length 45;  
Matches 27; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

436 GGTGTGCTTATGAGAGACGACGCGGTGGAACG 477

4 GGTGACGCGTTATGATGAAAAAATGCTAGTGTGTAGG 45

## LOCUS

AV832565 36 bp mRNA linear EST 22-JUN-2001

## DEFINITION

AV832565 K. Sato unpublished cDNA library: Hordeum vulgare subsp.  
vulgare leaves vegetative stage Hordeum vulgare subsp. vulgare cDNA

## ACCESSION

AV832565  
AV832565.1 GI:14524654

## VERSION

EST.

## KEYWORDS

Hordeum vulgare subsp. vulgare.  
Hordeum vulgare subsp. vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae  
; Triticeae; Hordeum.

## SOURCE

Sato, K.

## REFERENCE

Barley EST sequencing project in NIG and Okayama Univ  
Unpublished (2001)  
Contact: Kazuhiro Sato

## JOURNAL

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Email: kazsato@rib.okayama-u.ac.jp,  
URL: http://www.rib.okayama-u.ac.jp/barley/  
Sato, K.; Saito, D.; Takeda, K.; Shini, T. and Kohara, Y. Direct  
submission;  
database: http://www.shigen.nig.ac.jp/barley/Barley.html.

## FEATURES

Location/Qualifiers

1..36  
/organism="Hordeum vulgare subsp. vulgare"  
/cultivar="Akashinriki"  
/db\_xref="taxon:112509"  
/clone="ibaaki3h07"  
/clone\_lib="K. Sato unpublished cDNA library: Hordeum

vulgare subsp. vulgare leaves vegetative stage"  
/tissue\_type="leaves"  
/dev\_stage="vegetative stage"  
BASE COUNT 8 a 12 c 5 g 8 t 3 others  
ORIGIN

Query Match 1.6%; Score 17.8; DB 9; Length 36;  
Best Local Similarity 68.8%; Pred. No. 9e+05;  
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

184 AATTCTTGAAGCCTTGGATGACCTTGG 215

35 AATTGTGTAGCAGCCTTGAAGCAGCCTTGG 4

## LOCUS

R10619 36 bp mRNA linear EST 06-APR-1995

## DEFINITION

Yf35H1.r1 Soares fetal liver spleen INFILS Homo sapiens cDNA clone  
IMAGE:128901.5, similar to gb:L03840 FIBROBLAST GROWTH FACTOR  
RECEPTOR 4 PRECURSOR (HUMAN); mRNA sequence.

## ACCESSION

R10619  
R10619.1 GI:762575

## VERSION

EST.

## KEYWORDS

human.

## SOURCE

human.

## ORGANISM

human.

## REFERENCE

human.

## AUTHORS

human.

## TITLE

human.

## JOURNAL

human.

## COMMENT

human.

## FEATURES

human.

## SOURCE

human.

## LOCATION/QUALIFIERS

human.

## ORGANISM

human.

## CULTIVAR

human.

## DB\_XREF

human.

## CLONE

human.

## CLONE\_LIB

human.

## DEV\_STAGE

human.

## TISSUE\_TYPE

human.

## BASE\_COUNT

human.

## ORIGIN

human.

## Query Match

human.

## Best Local Similarity

human.





